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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:09:18 ; Search time 200 Seconds
(without alignments)
274.612 Million cell updates/sec

Title: US-10-661-784-2

Perfect score: 670
Sequence: 1 GSGKDFVQPPTRKICVGCPRD.....YVPMKKYPRVNCQPLGM 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1980s:.*
3: Geneseqp2000s:.*
4: Geneseqp2000s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003as:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	670	100.0	125	8	ADM16603 HK-D3v(GS
2	670	100.0	125	9	ADY71957 Variant h
3	660	98.5	123	3	AAV95426 Human hlg
4	660	98.5	123	9	ADM16602 Native HK
5	660	98.5	123	9	ADY71956 Native hu
6	660	98.5	268	8	ADP43683 Human PMW
7	660	98.5	268	8	ABM83721 Human dia
8	660	98.5	304	6	ABP70801 Human ext
9	660	98.5	304	6	ABM83720 Human dia
10	660	98.5	322	6	ABP70799 Human ext
11	660	98.5	326	6	ABM83717 Human dia
12	660	98.5	329	6	ABU92044 Human pro
13	660	98.5	329	6	ABM83716 Human dia
14	660	98.5	358	6	ABP70800 Human ext
15	660	98.5	362	9	ABE32339 Human pro
16	660	98.5	362	9	ABE32341 Human pro
17	660	98.5	390	6	ABU9149 Novel hum
18	660	98.5	390	8	ADM93863 Human NOV
19	660	98.5	390	8	ADT04032 Human pro
20	660	98.5	390	8	ADS93172 Novel hum
21	660	98.5	392	8	ABM83719 Human dia
22	660	98.5	398	6	ABU9143 Novel hum
23	660	98.5	398	6	ADM93851 Human NOV
24	660	98.5	398	8	ABM83718 Human dia

25	660	98.5	398	8	ADS93160 Novel hum
26	660	98.5	427	8	ADP76864 Human pro
27	660	98.5	427	8	ABM83715 Human dia
28	660	98.5	427	8	ABM80523 Tumour-as
29	660	98.5	427	8	ADQ39518 Human myo
30	660	98.5	427	8	ADQ39516 Human myo
31	660	98.5	427	8	ADS93164 Novel hum
32	660	98.5	579	9	ABE32342 Human pro
33	660	98.5	579	9	ABE32338 Human pro
34	660	98.5	615	6	ABU9144 Novel hum
35	660	98.5	615	6	ADM93142 Novel hum
36	660	98.5	615	8	ADM93853 Human NOV
37	660	98.5	615	8	ADS93162 Novel hum
38	660	98.5	616	8	ADS93154 Novel hum
39	660	98.5	621	8	ADS93156 Novel hum
40	660	98.5	621	8	ADS93184 Novel hum
41	660	98.5	622	8	ADS93158 Novel hum
42	660	98.5	626	5	ABP78707 Human hlg
43	660	98.5	626	8	ADH10413 Human hlg
44	660	98.5	644	4	ABG21101 Novel hum
45	660	98.5	644	5	ABP78710 Human hlg

ALIGNMENTS

RESULT 1
ADM16603 ADM16603 standard; protein; 125 AA.
XX AC ADM16603;
XX DT 17-JUN-2004 (first entry)
XX DE HK-D3v(GS) amino acid sequence, seq id 2.
XX KW Cytoplasmic; oncogenic; neuroprotective; antiparkinsonian; inhibitor;
KW cell migration; cell invasion; cell proliferation; angiogenesis;
KW apoptosis; tumour growth rate; human kininogen domain 3v; HK-D3v; HK-D3;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; mucin.
XX OS Homo sapiens.
XX OS Synthetic.
XX FN WO2004024877-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US028881.
XX PR 13-SEP-2002; 2002US-0410279P.
XX PA (ATTE-) ATTENUON LLC.
XX PI Donate F, Mazar A;
XX XX
XX WPI: 2004-270022/25.
XX DR N-PSDB; ADM16606.
XX PT Novel isolated anti-angiogenic polypeptide comprising sequence of human
PT kininogen domain 3v (HK-D3v) or variant of native HK-D3, useful for
PT inhibiting angiogenesis, endothelial cell proliferation or endothelial
PT tube formation.
XX PS Disclosure; SEQ ID NO 2; 79pp; English.
XX CC The invention relates to an isolated anti-angiogenic polypeptide (I)
CC comprising the sequence of human kininogen domain 3v (HK-D3v) (fully
CC defined sequence (S1) of 127 amino acids as given in specification) or
CC variant or derivative of native HK-D3 (fully defined sequence (S2) of 123
CC amino acids as given in specification), and has at least 20% of activity
CC of native HK-D3 in inhibiting angiogenesis, endothelial cell

CC proliferation or endothelial tube formation. Also disclosed is a
 CC diagnostically or therapeutically labeled anti-angiogenic polypeptide
 CC (ii) comprising (i) labeled with a diagnostic or therapeutic label, and
 CC a diagnostic HK-D3-related composition (iii) comprising (ii) labeled
 CC with a detectable label and a carrier. Further disclosed is an affinity
 CC ligand (ix) useful for binding to or isolating an HK-D3-binding molecule
 CC or cells expressing the binding molecule, comprising (i) immobilized to a
 CC solid support or carrier. (i) or (ii) are useful for inhibiting cell
 CC migration, cell invasion, cell proliferation or angiogenesis, or for
 CC inducing apoptosis which involves contacting cells associated with
 CC undesired cell migration, invasion, proliferation or angiogenesis with
 CC (i). (i) is useful for treating neurodegenerative diseases e.g.,
 CC Alzheimer's disease, Parkinson's disease or amyotrophic lateral sclerosis
 CC (ALS). The current sequence represents an N-terminal addition variant of
 CC HK-D3 designated HD-D3v(GS), that includes an additional GS at the N-
 CC terminus.

XX Sequence 125 AA;

Query Match 100.0%; Score 670; DB 8; Length 125;

Best Local Similarity 100.0%; Pred. No. 3.3e-67; Mismatches 0; Indels 0; Gaps 0;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSGKDFVQPPPTKICVGCPRDIPNTSPLEETLTHITTKLNANNATFYFKIDNVKKAQV 60

Db 1 GSGKDFVQPPPTKICVGCPRDIPNTSPLEETLTHITTKLNANNATFYFKIDNVKKAQV 60

Qy 61 VVAGKKYFIDFVARETTCKESNEELTESCETKLGOSLDCAEYVVPWEKKIYPTVNC 120

Db 61 VVAGKKYFIDFVARETTCKESNEELTESCETKLGOSLDCAEYVVPWEKKIYPTVNC 120

Qy 121 QPLGM 125

Db 121 QPLGM 125

RESULT 2
 ADY71957
 ID ADY71957 standard; protein; 125 AA.

XX ADY71957;

XX 02-JUN-2005 (first entry)

XX Variant human kininogen domain 3 HK-D3v(GS) protein.

XX protein engineering; kininogen; antiangiogenic; apoptosis; angiogenesis;

XX cancer; cytoskeletal.

XX Homo sapiens.

XX Synthetic.

XX US2005056599-A1.

XX 17-MAR-2005.

XX 15-SEP-2003; 2003US-00661784.

XX 15-SEP-2003; 2003US-00661784.

XX (DONA/) DONATE F.

XX (MAZA/) MAZAR A P.

XX Donate F, Mazar AP;

XX WPI; 2005-213544/22.

XX N-PSDB; ADY71960.

XX Novel human kininogen domain 3 variant inhibiting angiogenesis,
 PT endothelial cell proliferation or endothelial tube formation, useful for
 PT creating disease associated with undesired cell migration, invasion,
 PT proliferation or angiogenesis.

PS Disclosure; SEQ ID NO 2; 35pp; English.

XX The invention relates to an isolated anti-angiogenic polypeptide (I)
 CC having the sequence of human kininogen domain 3 variant (HK-D3v) having a
 CC fully defined 127 amino acid sequence given in the specification, or its
 CC variant or derivative, a variant or derivative of native HK-D3 having a
 CC fully defined 123 amino acid sequence given in the specification, which
 CC fully defined 123 amino acid sequence has at least 20% of the activity of
 CC native HK-D3 in inhibiting angiogenesis, endothelial cell proliferation
 CC or endothelial tube formation in an in vitro or in vivo bioassay. (i) is
 CC useful for inhibiting cell migration, cell invasion, cell proliferation
 CC or angiogenesis, or for inducing apoptosis, which involves contacting
 CC cells associated with (i) or a therapeutically labeled (i). A composition
 CC comprising (i) is useful for treating a subject having a disease or
 CC condition associated with undesired cell migration, invasion, proliferation
 CC proliferation or angiogenesis. (vi) or (vii) is useful for providing to a
 CC cell, tissue or organ an angiogenesis-inhibitory amount of HK-D3, HK-D3v
 CC or its variant. (i) is useful for treating cancer. This sequence
 CC corresponds to the variant HK-D3v(GS) protein which has an extra 2 amino
 CC acids (Gly-Ser) at the N-terminus of the HK-D3 protein (ADY71956).

XX Sequence 125 AA;

Query Match 100.0%; Score 670; DB 9; Length 125;

Best Local Similarity 100.0%; Pred. No. 3.3e-67; Mismatches 0; Indels 0; Gaps 0;

Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSGKDFVQPPPTKICVGCPRDIPNTSPLEETLTHITTKLNANNATFYFKIDNVKKAQV 60

Db 1 GSGKDFVQPPPTKICVGCPRDIPNTSPLEETLTHITTKLNANNATFYFKIDNVKKAQV 60

Qy 61 VVAGKKYFIDFVARETTCKESNEELTESCETKLGOSLDCAEYVVPWEKKIYPTVNC 120

Db 61 VVAGKKYFIDFVARETTCKESNEELTESCETKLGOSLDCAEYVVPWEKKIYPTVNC 120

Qy 121 QPLGM 125

Db 121 QPLGM 125

RESULT 3
 AA95426
 ID AA95426 standard; peptide; 123 AA.

XX AA95426;

XX 25-SEP-2000 (first entry)

XX Human high mol.wt. kininogen domain 3.

XX Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue;

XX endothelial cell proliferation; apoptosis; cancer; ocular disorder;

XX rheumatoid arthritis; cytoskeletal; antiarthritic; antiinflammatory;

XX human; D3 peptide.

XX Homo sapiens.

XX WO200035407-A2.

XX 22-JUN-2000.

XX 02-DEC-1999; 99WO-US028465.

XX 16-DEC-1998; 98US-0112427P.

XX (UTEM) UNIV TEMPLE.

XX (MCCR/) MCCRAE R K.

XX Mccrae RK;

XX WPI; 2000-442247/38.

PT Composition for inhibiting angiogenesis and endothelial cell
 PT proliferation, inducing endothelial cell apoptosis and treating cancer,
 PT rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3
 PT analog.

PS Disclosure; Page 4; 44pp; English.

CC The present sequence is that of domain 3 of human high mol. wt. kininogen
 CC (HK). The invention provides peptides (see AAY95405-24) that are
 CC analogues of certain sites in the HK domain 3, specifically Asn275-
 CC Lys282, Cys246-Cys249, Leu331-Tyr338 and Tyr239-Ser314. The peptides, in
 CC which native Cys residues may be replaced by Ala residues, inhibit
 CC endothelial cell proliferation and may also induce endothelial cell
 CC apoptosis. Compositions including the peptides are used in claimed
 CC methods for inhibiting angiogenesis, inhibiting endothelial cell
 CC proliferation, and inducing endothelial cell apoptosis. Cancer,
 CC rheumatoid arthritis, and ocular disorders characterized by undesired
 CC vascularization of the retina are treated

XX Sequence 123 AA;

Query Match 98.5%; Score 660; DB 3; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4,4e-66;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNTSPLEETLTHITTKLNAENNAATFYFKIDNVKARVQV 62
 DB 1 GKDVPQPTKICVGCPRDIPNTSPLEETLTHITTKLNAENNAATFYFKIDNVKARVQV 60

QY 63 AGKKYFIDFVARETTSKESNEBELTESCETKLGSLDCAEYVVPWEKKIYPTVNCOP 122
 DB 61 AGKKYFIDFVARETTSKESNEBELTESCETKLGSLDCAEYVVPWEKKIYPTVNCOP 120

QY- 123 LGM 125
 DB 121 LGM 123

QY- 123 LGM 125
 DB 121 LGM 123

RESULT 4
 ID ADM16602
 ID ADM16602 standard; protein, 123 AA.

AC ADM16602;

DT 17-JUN-2004 (first entry)

DE Native HK-D3 amino acid sequence, seq id 1.

XX Cytostatic; neurotropic; neuroprotective; antiparkinsonian; inhibitor;
 KW cell migration; cell invasion; cell proliferation; angiogenesis;
 KW apoptosis; tumour growth rate; human kininogen domain 3v; HK-D3v; HK-D3;
 KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS.

XX Homo sapiens.

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PT inhibiting angiogenesis, endothelial cell proliferation or endothelial
 PT tube formation.

XX Claim 1; SEQ ID NO 1; 79pp; English.

CC The invention relates to an isolated anti-angiogenic polypeptide (I)
 CC comprising the sequence of human kininogen domain 3v (HK-D3v) (fully
 CC defined sequence (S1) of 127 amino acids as given in specification) or
 CC variant or derivative of native HK-D3 (fully defined sequence (S2) of 123
 CC amino acids as given in specification), and has at least 20% of activity
 CC of native HK-D3 in inhibiting angiogenesis, endothelial cell
 CC proliferation or endothelial tube formation. Also disclosed is a
 CC diagnostic (I) therapeutically labelled anti-angiogenic polypeptide
 CC (II) comprising (I) labelled with a diagnostic or therapeutic label, and
 CC a diagnostic HK-D3-related composition (III) comprising (II) labelled
 CC with a detectable label and a carrier. Further disclosed is an affinity
 CC ligand (IX) useful for binding to or isolating an HK-D3-binding molecule
 CC or cells expressing the binding molecule, comprising (I) immobilized to a
 CC solid support or carrier. (I) or (II) are useful for inhibiting cell
 CC migration, cell invasion, cell proliferation or angiogenesis, or for
 CC inducing apoptosis which involves contacting cells associated with
 CC undesired cell migration, invasion, proliferation or angiogenesis with
 CC (I). (I) is useful for treating neurodegenerative diseases e.g.,
 CC Alzheimer's disease, Parkinson's disease or amyotrophic lateral sclerosis
 CC (ALS). The current sequence represents the native HK-D3 amino acid
 CC sequence.

XX Sequence 123 AA;

Query Match 98.5%; Score 660; DB 8; Length 123;
 Best Local Similarity 100.0%; Pred. No. 4,4e-66;

Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNTSPLEETLTHITTKLNAENNAATFYFKIDNVKARVQV 62
 DB 1 GKDVPQPTKICVGCPRDIPNTSPLEETLTHITTKLNAENNAATFYFKIDNVKARVQV 60

QY 63 AGKKYFIDFVARETTSKESNEBELTESCETKLGSLDCAEYVVPWEKKIYPTVNCOP 122
 DB 61 AGKKYFIDFVARETTSKESNEBELTESCETKLGSLDCAEYVVPWEKKIYPTVNCOP 120

QY- 123 LGM 125
 DB 121 LGM 123

QY- 123 LGM 125
 DB 121 LGM 123

RESULT 5
 ID ADY71956
 ID ADY71956 standard; protein, 123 AA.

AC ADY71956;

DT 02-JUN-2005 (first entry)

DE Native human kininogen domain 3 protein.

XX protein engineering; kininogen; antiangiogenic; apoptosis; angiogenesis;
 KW cancer; cytostatic.

XX Homo sapiens.

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Fri Feb 10 16:46:32 2006

XX WPI; 2005-213544/22.

Novel human kitinogen domain 3 variant inhibiting angiogenesis,
endothelial cell proliferation or endothelial tube formation, useful for
treating disease associated with undesired cell migration, invasion,
proliferation or angiogenesis.

Claim 1; SEQ ID NO 1; 35bp; English.

The invention relates to an isolated anti-angiogenic polypeptide (I) having the sequence of human kitinogen domain 3 variant (HK-D3) having a fully defined 127 amino acid sequence given in the specification, or its variant or derivative, a variant or derivative of native HK-D3 having a fully defined 123 amino acid sequence given in the specification, which polypeptide, variant or derivative has at least 20% of the activity of native HK-D3 in inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in an in vitro or in vivo bioassay. (I) is useful for inhibiting cell migration, cell invasion, cell proliferation or angiogenesis, or for inducing apoptosis, which involves contacting cells associated with undesired cell migration, invasion, proliferation or angiogenesis with (I) or a therapeutically labeled (I). A composition comprising (I) is useful for treating a subject having a disease or condition associated with undesired cell migration, invasion, proliferation or angiogenesis. (VI) or (VII) is useful for providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HK-D3, HK-D3v or its variant. (I) is useful for treating cancer. This sequence corresponds to the native HK-D3 protein sequence.

Sequence 123 AA:

Query Match 98.5%; Score 660; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. NO. 4.4e-66; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 GKDPIQPTKICVCGPRDIPNSPELETLTHITTKLAENNAATPYFKIDNVKARQV 62
1 GKDFQOPTKICVCGPRDIPNSPELETLTHITTKLAENNAATPYFKIDNVKARQV 60
63 AGKVFIFVARETTCSENEELTESCETKLGOSLDONAEVYVPMKKIYPTVNCOP 122
61 AGKVFIFVARETTCSENEELTESCETKLGOSLDONAEVYVPMKKIYPTVNCOP 120
123 LGM 125
121 LGM 123

RESULT 6
ADP43683 standard; protein: 268 AA.

ADP43683:
18-NOV-2004 (first entry)
Human PMNM-40 protein SEQ ID NO:40.
human, protein modification and maintenance molecule; PMNM;
gastrointestinal, cardiovascular; immunosuppressive; antiinflammatory;
cytotoxic; neuroprotective; gynaecological; gene therapy;
gastrointestinal disorder; cardiovascular disorder; autoimmune disorder;
inflammatory disorder; cell proliferative disorder;
developmental disorder; epithelial disorder; neurological disorder;
reproductive disorder.

OS Homo sapiens.
XX
XX MO2004053068-AA2.
XX 24-JUN-2004.
XX 03-DEC-2003; 2003WO-US038573.

XX 05-DEC-2002; 2002US-0431639P.
PR 17-DEC-2002; 2002US-0434315P.
PR 24-JAN-2003; 2003US-0442442P.
PR 30-JAN-2003; 2003US-0444141P.
PR 21-FEB-2003; 2003US-0449491P.

(INCY-) INCYTE CORP.

Becha SD, Hafalia AJA, Swarnakar A, Ramkumar J, Richardson TW,
Kable AR, Margulis JP, Khare R, Lee SY, Tran UK, Bhattacharya UG,
Burrill JD, Blake JJ, Ho A, Zheng W, Gao J, Chawla NK, Mason PM,
Jin P, Lee S;

WPI; 2004-468843/44.
N-PDSB; ADP43724.

New human protein modification and maintenance molecules and polynucleotides for diagnosing, preventing or treating diseases associated with aberrant protein expression, e.g. cardiovascular or cell proliferative disorders.

Claim 1; SEQ ID NO 40; 268bp; English.

The present sequence represents a human protein modification and maintenance molecule (PMNM) (I), designated PMNM-40. Also described: (1) an isolated polynucleotide encoding (I); (2) a recombinant polynucleotide in a plasmid or a promoter operably linked to the polynucleotide; (4) a composition comprising (I) and a recombinant polynucleotide; (5) (1); (3) a cell transformed with the recombinant polynucleotide; (6) transgenic organism comprising (I); (7) a target polynucleotide or (I) methods of producing (I); (8) a target polynucleotide or (I) specifically binds to (I); (9) detecting a target polynucleotide, an agonist in a sample; (10) compositions comprising the polypeptide, an agonist compound, an antagonist compound or an antibody, and an excipient; (9) treating diseases or conditions associated with decreased expression or overexpression of functional human PMNM; (10) screening for a compound that is effective as an agonist or antagonist of (I), that specifically binds to (I), that modulates the activity of (I), or is effective in altering expression of the target polynucleotide; (11) screening for a potential toxicity of a test compound; (12) a diagnostic test for a condition or disease associated with the expression of PMNM in a biological sample; (13) diagnosing a condition or disease associated with the expression of PMNM in a subject; (14) preparing a polyclonal or monoclonal antibody with the specificity of the antibody in (6); (15) a monoclonal or monoclonal antibody produced by the method in (14); (16) compositions comprising the polyclonal or monoclonal antibody, and a carrier; (17) generating an array comprising different nucleotide polynucleotides; and (18) an array comprising different nucleotide molecules affixed at distinct physical locations on a solid substrate, where at least one nucleotide molecule comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 CC contiguous nucleotides of the target polynucleotide. PMNM sequences have CC cytotoxic, neuroprotective and gynaecological activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating diseases or conditions associated with aberrant expression of PMNM, such as gastrintestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological or reproductive disorders. They may also be used for assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of PMNM. The PMNM or its fragments are also useful in screening compounds for effectiveness as agonist or antagonist of the polypeptide, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring and measuring protein-protein interactions, drug-target interactions, and gene expression profiles.

Sequence 268 AA:

Query Match 98.5%; Score 660; DB 8; Length 268;
Best Local Similarity 100.0%; Pred. NO. 1.3e-65; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GDDFVQPPFKICVGCPRDIPNTSPBLEETLTHITTKLAENNAATFYFKIDNVKARQVY 62
DB 94 GDDFVQPPFKICVGCPRDIPNTSPBLEETLTHITTKLAENNAATFYFKIDNVKARQVY 153
QY 63 AGKKYFIDPVARETTCSKESNEBELTESCETKLGSLDCNAEYVVPWEKKIYPTVNCOP 122
DB 154 AGKKYFIDPVARETTCSKESNEBELTESCETKLGSLDCNAEYVVPWEKKIYPTVNCOP 213
QY 123 LGM 125
DB 214 LGM 216
RESULT 7
ABM83721
ID ABM83721 strand; protein; 268 AA.
XX ABM83721;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pProtein SEQ ID NO:3970.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
XX Harthorn TR, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
XX Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
XX Perez CA, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton BS,
XX Xu Y, Kwong M, Policky JU, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
XX Pacury S, Shi X, Suarez CO;
XX
XX WPI; 2004-329368/30.
XX
XX N-PSDB; ACC42373.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 27; Page: 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dthp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germ-line
XX gene therapy. The present sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
XX Sequence 268 AA:
XX
XX Query Match 98.5%; Score 660; DB 8; Length 268;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-65;
XX Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GDDFVQPPFKICVGCPRDIPNTSPBLEETLTHITTKLAENNAATFYFKIDNVKARQVY 62
DB 94 GDDFVQPPFKICVGCPRDIPNTSPBLEETLTHITTKLAENNAATFYFKIDNVKARQVY 153
QY 63 AGKKYFIDPVARETTCSKESNEBELTESCETKLGSLDCNAEYVVPWEKKIYPTVNCOP 122
DB 154 AGKKYFIDPVARETTCSKESNEBELTESCETKLGSLDCNAEYVVPWEKKIYPTVNCOP 213
QY 123 LGM 125
DB 214 LGM 216
RESULT 8
ABP70801
ID ABP70801 strand; protein; 304 AA.
XX ABP70801;
XX
XX 26-AUG-2003 (first entry)
XX
XX Human extracellular messenger, EXMES-28.
XX
XX Human; extracellular messenger; EXMES; cytostatic; antidiabetic;
XX immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
XX endocrine disorder; cancer.
XX
XX Homo sapiens.
XX
XX WO2003018612-A2.
XX
XX 06-MAR-2003.
XX
XX 22-AUG-2002; 2002WO-US027213.
XX
XX 24-AUG-2001; 2001US-0314811P.
XX
XX 14-DEC-2001; 2001US-0340584P.
XX
XX 18-JAN-2002; 2002US-0350595P.
XX
XX 11-MAR-2002; 2002US-0363432P.
XX
XX 15-MAR-2002; 2002US-0364607P.
XX
XX 05-APR-2002; 2002US-0370761P.
XX
XX 24-JUN-2002; 2002US-0391378P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Dugan BM, Lee S, Baughn MR, Hafalia AJA, Walla NK, Elliott VS;
XX Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;
XX Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zedarjadian Y,
XX Richardson TW, Kabie AB, Chang H, Swarnakar A, Leht-Mason PM,
XX Ramkumar J;
XX
XX WPI; 2003-278643/27.
XX
XX N-PSDB; ACC42386.
XX
XX New human extracellular messenger (EXMES) polypeptide, useful for
XX preparing a composition for treating a disease associated with decreased
XX expression or overexpression of functional EXMES e.g. autoimmune
XX disorders or cancer.
XX
XX Claim 1; Page 207; 224pp; English.
XX
XX The present invention relates to novel human extracellular messenger
XX proteins (EXMES-1 to -28; ABP7074-ABP70801) and their coding sequences
XX (ACC42361-ACC42388). The proteins are useful for preparing a composition
XX for diagnosing or treating a disease or condition associated with

CC decreased expression or overexpression of functional EXMES e.g.
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or
 CC cancer

XX Sequence 304 AA;

Query March 98.5%; Score 660; DB 6; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.5e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPFNSPELETLTHITTKLAENNAATFYFKIDNVKARQVY 62
 DB 130 GKDFVQPTKICVGCPRDIPFNSPELETLTHITTKLAENNAATFYFKIDNVKARQVY 189
 QY 63 AGKRYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCOP 122
 DB 190 AGKRYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCOP 249
 QY 123 LGM 125
 DB 250 LGM 252

RESULT 9
 ABM83720
 ID ABM83720 standard; protein; 304 AA.

XX ABM83720;
 XX 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3969.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

XX MO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003MO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;

PI Mooney BM, Deleage AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;

PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vile UA, Kitron ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI; 2004-329368/30.

XX N-PSDB; ACN42372.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: the sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIP0 at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 304 AA;

Query March 98.5%; Score 660; DB 6; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.5e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPFNSPELETLTHITTKLAENNAATFYFKIDNVKARQVY 62
 DB 130 GKDFVQPTKICVGCPRDIPFNSPELETLTHITTKLAENNAATFYFKIDNVKARQVY 189
 QY 63 AGKRYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCOP 122
 DB 190 AGKRYFIDFVARETTCSKESNEELTESCETKKLGOSLDCNAEVYVVPWEKKIYPTVNCOP 249
 QY 123 LGM 125
 DB 250 LGM 252

RESULT 10
 ABP70799
 ID ABP70799 standard; protein; 322 AA.

XX ABP70799;

XX 26-AUG-2003 (first entry)

DE Human extracellular messenger, EXMES-26.

KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;

KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;

KW endocrine disorder; cancer.

OS Homo sapiens.

XX MO2003018612-A2.

XX 06-MAR-2003.

XX 22-AUG-2002; 2002MO-US027213.

XX 24-AUG-2001; 2001US-0314811P.

XX 14-DEC-2001; 2001US-0340584P.

XX 18-JUN-2002; 2002US-0350595P.

XX 11-MAR-2002; 2002US-0363432P.

XX 15-MAR-2002; 2002US-0364607P.

XX 05-APR-2002; 2002US-0370761P.

XX 24-JUN-2002; 2002US-0391378P.

XX (INCY-) INCYTE GENOMICS INC.

XX Duggan BM, Lee S, Baughn MR, Hafalia AD, Walla NK, Elliott VS;

PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;

PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebarijadian Y;

PI Richardson TW, Kable AE, Chang H, Swarnakar A, Leht-Mason EM;

PI Rankumar J;

XX WPI; 2003-278643/27.

XX N-PSDB; ACC42386.

XX New human extracellular messenger (EXMES) polypeptide, useful for
 PT preparing a composition for treating a disease associated with decreased

PT expression or overexpression of functional EXMES e.g. autoimmune
 PT disorders or cancer.
 XX
 XX
 PS Claim 1; Page 205-206; 224pp; English.
 XX
 CC The present invention relates to novel human extracellular messenger
 CC protein (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences
 CC (ACC42361-ACC42388). The proteins are useful for preparing a composition
 CC for diagnosing or treating a disease or condition associated with
 CC decreased expression or overexpression of functional EXMES e.g.
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or
 CC cancer
 CC
 XX Sequence 322 AA;
 SQ
 Query Match 98.5%; Score 660; DB 6; Length 322;
 Best Local Similarity 100.0%; Pred. No. 1.6e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GKDVPPTKICVCGCPDIPITNSPELEETLTHITTKNAENNAATFYFKIDNVKARVQV 62
 DB 148 GKDVPPTKICVCGCPDIPITNSPELEETLTHITTKNAENNAATFYFKIDNVKARVQV 207
 QY 63 AGKKYFIDFVARETTCSKESNEELTESCETKLGQSLDCNAEVYVVPWEKKIYPTVNCOP 122
 DB 208 AGKKYFIDFVARETTCSKESNEELTESCETKLGQSLDCNAEVYVVPWEKKIYPTVNCOP 267
 QY 123 LGM 125
 DB 268 LGM 270
 RESULT 11
 ABM83717
 ID ABM83717 standard; protein; 326 AA.
 AC
 XX ABM83717;
 XX
 DY 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic protein SEQ ID NO:3966.
 XX
 KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX
 OS Homo sapiens.
 XX
 PN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
 PI Hachthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL,
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitec UA, Kiron ES,
 PI Xu Y, Kong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
 PI Patry S, Shi X, Suarez CJ,
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN42369.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 326 AA;
 Query Match 98.5%; Score 660; DB 8; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.7e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GKDVPPTKICVCGCPDIPITNSPELEETLTHITTKNAENNAATFYFKIDNVKARVQV 62
 DB 152 GKDVPPTKICVCGCPDIPITNSPELEETLTHITTKNAENNAATFYFKIDNVKARVQV 211
 QY 63 AGKKYFIDFVARETTCSKESNEELTESCETKLGQSLDCNAEVYVVPWEKKIYPTVNCOP 122
 DB 212 AGKKYFIDFVARETTCSKESNEELTESCETKLGQSLDCNAEVYVVPWEKKIYPTVNCOP 271
 QY 123 LGM 125
 DB 272 LGM 274
 RESULT 12
 ABU92044
 ID ABU92044 standard; protein; 329 AA.
 AC
 XX ABU92044;
 XX
 DT 15-JUL-2003 (first entry)
 XX
 DE Human protein modification and maintenance molecule-24 (PMM-24).
 XX
 KM Human; protein modification and maintenance molecule; PMM; cancer;
 KM cell proliferation disorder; atherosclerosis; neurological disorder;
 KM epilepsy; Huntington's disease; stroke; immune disorder; allergy;
 KM inflammatory disorder; AIDS; developmental disorder; hypothyroidism;
 KM Cushing's syndrome; gastrointestinal disorder; epithelial disorder;
 KM infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
 KM neuroprotective; cerebroprotective; anti-HIV; antiallergic; vulnerary;
 KM antiinflammatory; thymimetic.
 KM
 OS Homo sapiens.
 XX
 PN WO2003031939-A2.
 PD 17-APR-2003.
 PF 11-OCT-2002; 2002WO-US032850.
 PR 12-OCT-2001; 2001US-0329689P.
 PR 25-OCT-2001; 2001US-0335703P.
 PR 09-NOV-2001; 2001US-0348887P.
 PR 28-NOV-2001; 2001US-0334145P.
 PR 06-DEC-2001; 2001US-0337451P.
 PR 14-DEC-2001; 2001US-0340584P.
 XX

(INCY-) INCYTE GENOMICS INC.

PA Ramkumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;
 XX Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;
 PI Sprague JW, Hafalla AJA, Chawla NK, Lehr-Mason JM, Kable AE, Yue H;
 PI Margus JP, Yao MG, Richardson TW, Tang TY, Jin P, Chlen D;
 PI Bhalla U, Burrill JD, Lee S, Blake JU, Ho A, Zheng W;
 XX WPI; 2003-430274/40.
 DR N-PSDB; ACN42439.

XX New human protein modification and maintenance molecules (PMMW), useful
 XX for diagnosing, treating and preventing diseases or conditions associated
 PT with the aberrant PMMW expression e.g. cancer, atherosclerosis, or
 PT infections.

PS Claim 1; Page 264-265; 311pp; English.

XX The present invention relates to the isolation of human protein
 CC modification and maintenance molecules (PMMW), and the polynucleotide
 CC sequences encoding them. A total of 40 PMMW polypeptides (designated PMW
 CC -1 to PMMW-40) are disclosed. The sequences of the invention are useful
 CC for diagnosing a condition or disease associated with the expression of
 CC PMMW in a subject, preparing a polyclonal or monoclonal antibody, and
 CC generating an expression profile of a sample containing the
 CC polynucleotides. The diseases or conditions associated with decreased
 CC expression or overexpression of PMMW are cell proliferation disorders
 CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,
 CC Huntington's disease, stroke), immune/inflammatory disorders, (e.g. AIDS,
 CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's
 CC syndrome), gastrointestinal or epithelial disorders, and infections. The
 CC PMMW polypeptides or their fragments are useful in screening compounds
 CC for effectiveness as agonists or antagonists of the polypeptides, or in
 CC altering the expression of the target polynucleotide and compounds that
 CC specifically bind to, or modulate the activity of the polypeptide.
 CC ABU92021-ABU92060 represent the human PMMW polypeptides of the invention
 XX

XX Sequence 329 AA;
 SQ

Query Match 98.5%; Score 660; DB 6; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.7e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPITNSPELEETLTHITTKLNAENNAFFPKIDNVKKARQVV 62
 DB 155 GKDVPPTKICVGCPRDIPITNSPELEETLTHITTKLNAENNAFFPKIDNVKKARQVV 214

QY 63 AGKKYPTDFVARETTCKESNEBELTESCETKKGQSIDCNAEYVVPWEKKIYPTVNCOP 122
 DB 215 AGKKYPTDFVARETTCKESNEBELTESCETKKGQSIDCNAEYVVPWEKKIYPTVNCOP 274

QY 123 LGM 125
 DB 275 LGM 277

RESULT 13
 ABM63716
 ID ABM63716 standard; protein; 329 AA.

XX 18-NOV-2004 (first entry)
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3965.
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
 XX Homo sapiens.
 XX OS
 XX PN WO2004023973-A2.
 XX PD 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.
 PF 12-SEP-2002; 2002US-0410259P.
 XX 12-SEP-2002; 2002US-0410260P.
 PR 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.
 PA Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 XX Harthorne TA, Suchorolski MT, Altus CM, Pits SJ, Elder LV;
 PI Mooney EM, Delemane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gitzen D;
 PI Patruy S, Shi X, Suarez CJ;
 XX WPI; 2004-329368/30.
 DR N-PSDB; ACN42368.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC polynucleotide and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders, endocrine
 CC autoimmune/inflammatory disorders, gastrointestinal disorders, or
 CC infection caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WFO at www.wipo.int/pct/en/sequences/listing.htm
 XX

XX Sequence 329 AA;
 SQ

Query Match 98.5%; Score 660; DB 8; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.7e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPITNSPELEETLTHITTKLNAENNAFFPKIDNVKKARQVV 62
 DB 155 GKDVPPTKICVGCPRDIPITNSPELEETLTHITTKLNAENNAFFPKIDNVKKARQVV 214

QY 63 AGKKYPTDFVARETTCKESNEBELTESCETKKGQSIDCNAEYVVPWEKKIYPTVNCOP 122
 DB 215 AGKKYPTDFVARETTCKESNEBELTESCETKKGQSIDCNAEYVVPWEKKIYPTVNCOP 274

QY 123 LGM 125
 DB 275 LGM 277

RESULT 14
 ABP70800
 ID ABP70800 standard; protein; 358 AA.

XX 26-AUG-2003 (first entry)
 DE Human extracellular messenger, EXMES-27.
 XX

KW Human; extracellular messenger; EXMES; cytosolic; antidiabetic;
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;
 KW endocrine disorder; cancer.
 OS Homo sapiens.
 XX WO2003018612-A2.
 XX PD 06-MAR-2003.
 XX PF 22-AUG-2002; 2002WO-US027213.
 XX PR 24-AUG-2001; 2001US-0314811P.
 XX PR 14-DEC-2001; 2001US-0340584P.
 XX PR 18-JAN-2002; 2002US-0350595P.
 XX PR 11-MAR-2002; 2002US-0363432P.
 XX PR 15-MAR-2002; 2002US-0364607P.
 XX PR 05-APR-2002; 2002US-0370761P.
 XX PR 24-JUN-2002; 2002US-0391378P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Duggan BM, Lee S, Baughn MR, Hafalia AJA, Wajia NK, Elliott VS,
 PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N,
 PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zabarjadian Y,
 PI Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM,
 PI Rankumar J,
 XX WPI: 2003-278643/27.
 XX DR N-PSDB; ACC42387.
 XX PT New human extracellular messenger (EXMES) polypeptide, useful for
 PT preparing a composition for treating a disease associated with decreased
 PT expression or overexpression of functional EXMES e.g. autoimmune
 PT disorders or cancer.
 XX PS Claim 1, Page 206; 224p; English.
 XX CC The present invention relates to novel human extracellular messenger
 CC proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences
 CC (ACC42361-ACC42388). The proteins are useful for preparing a composition
 CC for diagnosing or treating a disease or condition associated with
 CC decreased expression or overexpression of functional EXMES e.g.
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or
 CC cancer
 CC CC
 SO Sequence 358 AA;
 Query Match 98.5%; Score 660; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 1.9e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GKDFVQPPPTKICVGCPRDIPNPSPELEETLTHITTKNAENNAFFYKIDNVKARQV 62
 DB 184 GKDFVQPPPTKICVGCPRDIPNPSPELEETLTHITTKNAENNAFFYKIDNVKARQV 243
 QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKLGQSLDCNAEYVYVPEKKIYPTVNCOP 122
 DB 244 AGKKYFIDFVARETTCKESNEBELTESCETKLGQSLDCNAEYVYVPEKKIYPTVNCOP 303
 QY 123 LGM 125
 DB 304 LGM 306

RESULT 15
 AEB32339
 ID AEB32339 standard; protein; 362 AA.
 XX
 AC AEB32339;
 XX
 DT 08-SEP-2005 (first entry)
 XX

DE Human protein #41.
 XX SNP detection; diagnosis; non-insulin dependent diabetes; obesity;
 KW antidiabetic; anorectic; endocrine disease; gastrointestinal disease;
 KW metabolic disorder; nutritional disorder.
 OS Homo sapiens.
 XX US2005147987-A1.
 XX PN 07-JUL-2005.
 XX PD 19-JUL-2004; 2004US-00893315.
 XX PF 08-SEP-2000; 2000US-0231397P.
 XX PR 10-SEP-2001; 2001US-00948947.
 XX PA (APPL-) APPLERA CORP NY.
 XX PI Venter JC, Zhang JN, Liu X, Rowe W, Cravchik A, Kalush F,
 PI Naik A, Subramanian G, Woodage T;
 XX WPI: 2005-511776/52.
 XX DR N-PSDB; AEB32278.
 XX PT New detection reagent capable of detecting 1, 100, 500, 1000 or 5000 or
 PT more single nucleic acid polymorphisms, useful in identifying an
 PT individual having or at risk of developing type II diabetes or obesity.
 XX PS Disclosure; SEQ ID NO 102; 31pp; English.
 XX CC The invention relates to a detection reagent capable of detecting one or
 CC more single nucleic acid polymorphisms. The invention also relates to
 CC determining whether a trait is linked to one of the human chromosomes or
 CC its sub-region, a computer readable medium having stored in it the SNP
 CC relational information given in the specification, an isolated nucleic
 CC acid molecule for detecting at least one SNP given in the specification
 CC comprising at least about 12 contiguous nucleotides, genotyping at least
 CC one SNP position given in the specification in a sample, identifying an
 CC individual having or at risk of developing a disorder and a kit
 CC comprising at least one container containing the detection reagent.
 CC Determining whether a trait is linked to one of the human chromosomes or
 CC its sub-region comprises determining whether the trait is linked to one
 CC or more SNPs using the detection reagents. Genotyping at least one SNP
 CC position given in the specification in a sample comprises contacting the
 CC sample with a detection reagent that differentiates between alternative
 CC alleles at at least one SNP position given in the specification, and
 CC determining which allele is present at the at least one SNP position.
 CC Identifying an individual having or at risk of developing a disorder
 CC comprises genotyping at least one SNP given in the specification in a
 CC nucleic acid sample from the individual. The disorder is type II diabetes
 CC (non-insulin dependent diabetes) or obesity. The detection reagent is
 CC useful in identifying an individual having or at risk of developing a
 CC disorder, particularly type II diabetes or obesity. This sequence
 CC represents a human protein used in the scope of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 SO Sequence 362 AA;
 Query Match 98.5%; Score 660; DB 9; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.9e-65;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GKDFVQPPPTKICVGCPRDIPNPSPELEETLTHITTKNAENNAFFYKIDNVKARQV 62
 DB 188 GKDFVQPPPTKICVGCPRDIPNPSPELEETLTHITTKNAENNAFFYKIDNVKARQV 247
 QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKLGQSLDCNAEYVYVPEKKIYPTVNCOP 122
 DB 248 AGKKYFIDFVARETTCKESNEBELTESCETKLGQSLDCNAEYVYVPEKKIYPTVNCOP 307

Fri Feb 10 16:46:32 2006

us-10-661-784-2.rag

Page 10

Qy	123	LGM	125
Db	308	LGM	310

Search completed: February 8, 2006, 03:12:51
Job time : 202 secs

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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:17:23 ; Search time 48 Seconds
(Without alignments)
215.301 Million cell updates/sec

Title: US-10-661-784-2

Perfect score: 670

Sequence: 1 GSGKQPVQPTKICVGCPRD.....YVPMKRIYPTVNCPLGM 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/aa/8 COMB.pep:*
4: /cgn2_6/prodata/1/aa/PCUS_COMB.pep:*
5: /cgn2_6/prodata/1/aa/RE_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	98.5	123	2	US-09-461-061-18 Sequence 18, Appl
2	660	98.5	362	2	US-09-949-002-476 Sequence 476, App
3	660	98.5	362	2	US-09-949-002-480 Sequence 480, App
4	660	98.5	427	2	US-09-919-039-29 Sequence 29, Appl
5	660	98.5	579	2	US-09-949-002-475 Sequence 475, App
6	660	98.5	579	2	US-09-949-002-481 Sequence 481, App
7	600	89.6	117	1	US-08-193-114B-1 Sequence 1, Appl
8	594	88.7	117	4	PCR-US92-06809-1 Sequence 1, Appl
9	169	25.2	178	1	US-08-791-522-1 Sequence 1, Appl
10	169	25.2	178	2	US-09-314-777-1 Sequence 1, Appl
11	166	24.8	32	2	US-09-461-061-17 Sequence 17, Appl
12	165.5	24.7	145	1	US-08-832-535-2 Sequence 2, Appl
13	165.5	24.7	145	2	US-09-019-485-2 Sequence 2, Appl
14	165.5	24.7	145	2	US-09-019-485-3 Sequence 3, Appl
15	165.5	24.7	145	2	US-09-431-480-9 Sequence 9, Appl
16	165.5	24.7	145	2	US-09-617-302-9 Sequence 9, Appl
17	165.5	24.7	145	2	US-09-528-436B-2 Sequence 2, Appl
18	161	24.0	32	2	US-09-461-061-4 Sequence 4, Appl
19	155	23.1	27	2	US-08-676-242-11 Sequence 11, Appl
20	153	22.8	27	2	US-09-461-061-8 Sequence 8, Appl
21	145	21.6	64	2	US-08-676-242-22 Sequence 22, Appl
22	145	21.6	64	2	US-09-402-732-1 Sequence 1, Appl
23	138.5	20.7	121	2	US-09-775-932-14 Sequence 14, Appl
24	138.5	20.7	128	1	US-09-775-932-12 Sequence 12, Appl
25	138.5	20.7	149	1	US-08-461-030C-2 Sequence 2, Appl
26	138.5	20.7	149	2	US-08-744-138-2 Sequence 2, Appl
27	138.5	20.7	149	2	US-09-431-480-8 Sequence 8, Appl

28	138.5	20.7	149	2	US-09-431-480-10 Sequence 10, Appl
29	138.5	20.7	149	2	US-09-617-302-8 Sequence 8, Appl
30	138.5	20.7	149	2	US-09-617-302-10 Sequence 10, Appl
31	138.5	20.7	149	2	US-09-241-376-2 Sequence 2, Appl
32	138.5	20.7	149	2	US-09-940-497-2 Sequence 2, Appl
33	136.5	20.3	112	2	US-08-849-303-16 Sequence 16, Appl
34	135	20.1	118	2	US-09-775-932-24 Sequence 24, Appl
35	134	20.0	148	4	PCR-US95-07135-2 Sequence 2, Appl
36	132	19.7	26	2	US-08-676-242-15 Sequence 15, Appl
37	130	19.4	127	2	US-08-849-303-19 Sequence 19, Appl
38	129.5	19.3	140	2	US-09-886-319A-46 Sequence 46, Appl
39	129.5	19.3	140	2	US-09-886-319A-48 Sequence 48, Appl
40	129.5	19.3	314	2	US-09-949-016-11341 Sequence 11341, A
41	129.5	19.3	382	2	US-09-599-360B-93 Sequence 93, Appl
42	128.5	19.2	146	6	5432264-6 Patent No. 5432264
43	128	19.1	111	2	US-08-849-303-26 Sequence 26, Appl
44	127.5	19.0	120	2	US-09-775-932-2 Sequence 2, Appl
45	127.5	19.0	140	2	US-09-431-480-5 Sequence 5, Appl

ALIGNMENTS

```

RESULT 1
US-09-461-061-18
; Sequence 18, Application US/09461061
; Patent No. 6869931
; GENERAL INFORMATION:
; APPLICANT: McCrae, Keith R.
; TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
; TITLE OF INVENTION: Kithogen Domain 3 Peptide Analogs
; FILE REFERENCE: 6056-260 US
; CURRENT APPLICATION NUMBER: US/09/461, 061
; EARLIER FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,427
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human HK
; OTHER INFORMATION: domain 3
US-09-461-061-18
Query Match          98.5%; Score 660; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 GSDVQPPFKICVGCPRDIPNTPLEETLTHTITKLNANNATYFKIDNVKARQVY 62
      |||
Db      1 GSDVQPPFKICVGCPRDIPNTPLEETLTHTITKLNANNATYFKIDNVKARQVY 60
QY      63 AKKTPRIDVAETTCCKSNSELTSCCTKLGSLDGNNAVYVPMKRIYPTVNCPL 122
      |||
Db      61 AKKTFRIDVAETTCCKSNSELTSCCTKLGSLDGNNAVYVPMKRIYPTVNCPL 120
QY      123 LGM 125
      |||
Db      121 LGM 123

RESULT 2
US-09-949-002-476
; Sequence 476, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF

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FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 476
LENGTH: 362
TYPE: PRF
ORGANISM: Human
US-09-949-002-476

Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-65; Length 362;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 62
DB 188 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 247
QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 122
DB 248 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 307
QY 123 LGM 125
DB 308 LGM 310

RESULT 3
US-09-949-002-480
Sequence 480, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 480
LENGTH: 362
TYPE: PRF
ORGANISM: Human
US-09-949-002-480

Query Match
Best Local Similarity 100.0%; Pred. No. 4.3e-65; Length 362;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 62
DB 188 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 247
QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 122
DB 248 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 307
QY 123 LGM 125
DB 308 LGM 310

RESULT 4
US-09-919-039-29
Sequence 29, Application US/09919039
Patent No. 6727066

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 29
LENGTH: 427
TYPE: PRF
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 167507CD1
US-09-919-039-29

Query Match
Best Local Similarity 100.0%; Pred. No. 5.3e-65; Length 427;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 62
DB 253 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 312
QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 122
DB 313 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 372
QY 123 LGM 125
DB 373 LGM 375

RESULT 5
US-09-949-002-475
Sequence 475, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 475
LENGTH: 579
TYPE: PRF
ORGANISM: Human
US-09-949-002-475

Query Match
Best Local Similarity 100.0%; Pred. No. 8e-65; Length 579;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 62
DB 188 GKDFVQPTKICVGCPRDIPITNSPELEETLTHITTKLAENNAATFYFKIDNVKKARQV 247
QY 63 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 122
DB 248 AGKKYFIDFVARETTCKESNEBELTESCETKKGQSIDCAAEVYVVPWEKKIYPTVNCOP 307
QY 123 LGM 125
DB 308 LGM 310

RESULT 6

US-09-949-002-481

Sequence 481, Application US/09949002

Patent No. 6900016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

FILE REFERENCE: CLO00790

CURRENT APPLICATION NUMBER: US/09/949,002

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/231,401

NUMBER OF SEQ ID NOS: 10823

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 481

LENGTH: 579

TYPE: PRT

ORGANISM: Human

US-09-949-002-481

Query Match 98.5%; Score 660; DB 2; Length 579;

Best Local Similarity 100.0%; Pred. No. 8e-65; Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPNTSPLEETLTHITTKLMAENNAFFYFKIDNVKARQV 62

DB 188 GKFVGPPTKICVGCPRDIPNTSPLEETLTHITTKLMAENNAFFYFKIDNVKARQV 247

QZ 63 AGKKYIDFVARTTSGKESNEBLTSCETKLGOSLDCAEYVVPWEKKIYPTVNCOP 122

DB 248 AGKKYIDFVARTTSGKESNEBLTSCETKLGOSLDCAEYVVPWEKKIYPTVNCOP 307

QY 123 LGM 125

DB 308 LGM 310

RESULT 7

US-08-193-114B-1

Sequence 1, Application US/08193114B

Patent No. 5472945

GENERAL INFORMATION:

APPLICANT: Schmaier, Alvin H.

TITLE OF INVENTION: Modulation of Blood

TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavoragna &

ADDRESS: Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/193,114B

FILING DATE: 9 February 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Application

APPLICATION NUMBER: Serial No. 5472945 07/744,545

FILING DATE: 13 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-137 C11

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5472945e

INFORMATION FOR SEQ ID NO: 1;

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: peptide

TOPOLOGY: linear

US-08-193-114B-1

Query Match 89.6%; Score 600; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 4.5e-59; Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CVGCPDIPNTSPLEETLTHITTKLMAENNAFFYFKIDNVKARQVAGKKYIDFVA 73

DB 1 CVGCPDIPNTSPLEETLTHITTKLMAENNAFFYFKIDNVKARQVAGKKYIDFVA 60

QY 74 RETTCKESNEBLTSCETKLGOSLDCAEYVVPWEKKIYPTVNCOP LGM 125

DB 61 RETTCKESNEBLTSCETKLGOSLDCAEYVVPWEKKIYPTVNCOP LGM 112

RESULT 8

PCT-US92-06809-1

Sequence 1, Application PC/TUS9206809

GENERAL INFORMATION:

APPLICANT: Schmaier, Alvin H.

TITLE OF INVENTION: Modulation of Blood

TITLE OF INVENTION: Pressure by Altering Bradykinin Levels

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of the

ADDRESS: Commonwealth System of Higher Education

STREET: 406 University Services

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/06809

FILING DATE: 19910813

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Application

APPLICATION NUMBER: Serial No. 744,545

FILING DATE: 13 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-137

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

PCT-US92-06809-1

Query Match 88.7%; Score 594; DB 4; Length 117;
Best Local Similarity 98.2%; Pred. No. 2,1e-58;
Matches 110; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 CVGCPDIPNPSPELEETLTHITTKLNAENNATFYFKIDNVKARQVAVGKYYFIDEVA 73
DB 1 CVGCPDIPNPSPELEETLTHITTKLNAENNATFYFKIDNVKARQVAVGKYYFIDEVA 60
QY 74 RETTCKESNEBELTESCETKGLGSLDQNAEVVYVPEKKIYPTVNCOPJGM 125
DB 61 RETTCKESNEBELTESCETKGLGSLDQNAEVVYVPEKKIYPTVNCOPJGM 112

RESULT 9
US-08-791-522-1
Sequence 1, Application US/08791522
Patent No. 5935817
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/791,522
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-08-791-522-1

Query Match 25.2%; Score 169; DB 1; Length 178;
Best Local Similarity 32.5%; Pred. No. 7,2e-11;
Matches 39; Conservative 22; Mismatches 49; Indels 10; Gaps 4;

QY 11 TKICVCGPRDIPNPSPELEETLTHITTKLNAENNATFYFKIDNVKARQVAVGKYYFID 70
DB 54 SRVKGPEFKTKTNDPGVLAARYSVEKFNCTDMFLFKSRTTRALVQIVGKXTMLE 113
QY 71 FVARETTCKESNEBELTESC---TKKLGSLDQNAEVVYVPEKKIYPTVN--COPJGM 125
DB 114 VEIGRTTCKKQKQHLRL-DCCDFQTNHTLKQTLSCYSEVWVPW----VPALRGACSPJSL 168

RESULT 10
US-09-314-777-1
Sequence 1, Application US/09314777
Patent No. 6110686
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,777
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/791,522
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0193 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 30443
US-09-314-777-1

Query Match 25.2%; Score 169; DB 2; Length 178;
Best Local Similarity 32.5%; Pred. No. 7,2e-11;
Matches 39; Conservative 22; Mismatches 49; Indels 10; Gaps 4;

QY 11 TKICVCGPRDIPNPSPELEETLTHITTKLNAENNATFYFKIDNVKARQVAVGKYYFID 70
DB 54 SRVKGPEFKTKTNDPGVLAARYSVEKFNCTDMFLFKSRTTRALVQIVGKXTMLE 113
QY 71 FVARETTCKESNEBELTESC---TKKLGSLDQNAEVVYVPEKKIYPTVN--COPJGM 125
DB 114 VEIGRTTCKKQKQHLRL-DCCDFQTNHTLKQTLSCYSEVWVPW----VPALRGACSPJSL 168

RESULT 11
US-09-461-061-17
Sequence 17, Application US/09461061
Patent No. 6869931
GENERAL INFORMATION:
APPLICANT: McGee, Keith R.
TITLE OF INVENTION: Inhibition of Angiogenesis By High Molecular Weight
FILE REFERENCE: 6056-260 US
CURRENT APPLICATION NUMBER: US/09/461,061
CURRENT FILING DATE: 1999-12-15
EARLIER APPLICATION NUMBER: 60/112,427
EARLIER FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 21

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Analog of
US-09-461-061-17

Query Match 24.8%; Score 166; DB 2; Length 32;
Best Local Similarity 96.9%; Pred. No. 1.6e-11;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 87 TESCETKLGQSLDCNAEYVYVPEKKIYPTV 118
Db 1 TESCETKLGQSLDCNAEYVYVPEKKIYPTV 32

RESULT 12
US-08-832-535-2
Sequence 2, Application US/08832535
Patent No. 5919658
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: LI, HAODONG
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L
TITLE OF INVENTION: HUMAN CYSTATIN F
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,535
FILING DATE: 03-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIMBALL, PAUL C.
REGISTRATION NUMBER: 34,610
REFERENCE/DOCKET NUMBER: PP265
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 994-1700
TELEFAX: (201) 994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-832-535-2

Query Match 24.7%; Score 165.5; DB 1; Length 145;
Best Local Similarity 32.5%; Pred. No. 1.3e-10;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

Qy 11 TKICVGCPRDIPNPSLEETLHTITKLNANNATFYFIDNVKARVOVVGKKYFID 70
Db 32 SRVKGPFPTIKTNDGVLOARISVEKFNCTNDMFLFKESRITRALVQIVGKLTMLE 91

Qy 71 FVARETTCKSKESNEELTESCE--TKLQGSIDCNAEYVYVPEKKI-YPTVNC 120
Db 92 VEIGRTTCKKQKQRLR-DDCDFTNHTLKQTLSCYSEVWVVPMLQHFVEVPLAC 144

RESULT 13
US-09-019-485-2
Sequence 2, Application US/09019485
Patent No. 6066617
GENERAL INFORMATION:
APPLICANT: LI, Haodong
APPLICANT: YU, Guo-Liang
APPLICANT: GENTZ, Reiner
APPLICANT: NI, Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,485
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF265P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098439
TELEFAX: 3013098504
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-485-2

Query Match 24.7%; Score 165.5; DB 2; Length 145;
Best Local Similarity 32.5%; Pred. No. 1.3e-10;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

Qy 11 TKICVGCPRDIPNPSLEETLHTITKLNANNATFYFIDNVKARVOVVGKKYFID 70
Db 32 SRVKGPFPTIKTNDGVLOARISVEKFNCTNDMFLFKESRITRALVQIVGKLTMLE 91

Qy 71 FVARETTCKSKESNEELTESCE--TKLQGSIDCNAEYVYVPEKKI-YPTVNC 120
Db 92 VEIGRTTCKKQKQRLR-DDCDFTNHTLKQTLSCYSEVWVVPMLQHFVEVPLAC 144

RESULT 14
US-09-019-485-3
Sequence 3, Application US/09019485
Patent No. 6066617
GENERAL INFORMATION:
APPLICANT: LI, Haodong
APPLICANT: YU, Guo-Liang
APPLICANT: GENTZ, Reiner
APPLICANT: NI, Jian
TITLE OF INVENTION: Cystatin F
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: US

Search completed: February 8, 2006, 03:18:49
Job time : 48 secs

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; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,485
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Robert H.
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PF265P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3013098504
; TELEFAX: 3013098439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-019-485-3
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Query Match 24.7%; Score 165.5; DB 2; Length 145;
Best Local Similarity 32.5%; Pred. No. 1.3e-10;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

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QY 71 FVAARETTCSKESNEELTESCE--TKLGGSLDCNAEYVVVPMWEKI-YPTVNC 120
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Db 92 VEIGRTTCKKQNHRL-DDCDFOTNHTLKQTLSCYSEVWVWVPMLOHFEVPLRC 144
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US-09-431-480-9
; Sequence 9, Application US/09431480
; Patent No. 6235708
; GENERAL INFORMATION:
; APPLICANT: Hollaway, James L.
; TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
; FILE REFERENCE: 98-72
; CURRENT APPLICATION NUMBER: US/09/431,480
; EARLIER FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 60/109,217
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/156,382
; EARLIER FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-480-9
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Query Match 24.7%; Score 165.5; DB 2; Length 145;
Best Local Similarity 32.5%; Pred. No. 1.3e-10;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

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QY 11 TKICVGCPRDIPITNSPELEETLTHTITKLAENNAATFYFKIDNVKARVQVAVGKYYFID 70
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Db 32 SRVKGPFKTIKTNDPGVLQARYSVEKFNNTCTNDMFLFKESRITRALVQIVGKIKYMLE 91
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QY 71 FVAARETTCSKESNEELTESCE--TKLGGSLDCNAEYVVVPMWEKI-YPTVNC 120
   |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 92 VEIGRTTCKKQNHRL-DDCDFOTNHTLKQTLSCYSEVWVWVPMLOHFEVPLRC 144
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:18:07 ; Search time 179 Seconds
(without alignments)
291.780 Million cell updates/sec

Title: US-10-661-784-2
Perfect score: 670
Sequence: 1 GSGKDFVQPTKICVGCPRD.....YVPMKKIYPTVNCQPLGM 125

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications MA Main:

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2: /cgn2_6/ptodata/1/pubdae/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubdae/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubdae/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubdae/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubdae/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	670	100.0	125	US-10-661-784-2	Sequence 2, Appl1
2	660	98.5	123	US-10-661-784-1	Sequence 1, Appl1
3	660	98.5	362	US-10-893-315-102	Sequence 102, App
4	660	98.5	362	US-10-893-315-104	Sequence 104, App
5	660	98.5	390	US-10-162-335-82	Sequence 82, Appl
6	660	98.5	390	US-10-637-313-32	Sequence 32, Appl
7	660	98.5	398	US-10-162-335-70	Sequence 70, Appl
8	660	98.5	398	US-10-637-313-20	Sequence 20, Appl
9	660	98.5	427	US-09-919-039-29	Sequence 29, Appl
10	660	98.5	427	US-10-637-313-24	Sequence 24, Appl
11	660	98.5	427	US-10-741-600-1179	Sequence 1179, Ap
12	660	98.5	427	US-10-741-600-1181	Sequence 1181, Ap
13	660	98.5	579	US-10-893-315-101	Sequence 101, App
14	660	98.5	579	US-10-893-315-105	Sequence 105, App
15	660	98.5	615	US-10-162-335-72	Sequence 72, Appl
16	660	98.5	615	US-10-637-313-32	Sequence 32, Appl
17	660	98.5	616	US-10-637-313-14	Sequence 14, Appl
18	660	98.5	621	US-10-637-313-16	Sequence 16, Appl
19	660	98.5	621	US-10-637-313-44	Sequence 44, Appl
20	660	98.5	622	US-10-637-313-18	Sequence 18, Appl
21	660	98.5	626	US-10-507-734-25	Sequence 25, Appl
22	660	98.5	644	US-10-162-335-74	Sequence 74, Appl
23	660	98.5	644	US-10-162-335-84	Sequence 84, Appl
24	660	98.5	644	US-10-637-313-2	Sequence 2, Appl1
25	660	98.5	644	US-10-637-313-4	Sequence 4, Appl1
26	660	98.5	644	US-10-637-313-6	Sequence 6, Appl1
27	660	98.5	644	US-10-637-313-52	Sequence 52, Appl

28	660	98.5	644	5	US-10-637-313-54	Sequence 54, Appl
29	660	98.5	644	5	US-10-637-313-56	Sequence 56, Appl
30	660	98.5	644	5	US-10-637-313-58	Sequence 58, Appl
31	660	98.5	644	5	US-10-637-313-60	Sequence 60, Appl
32	660	98.5	644	5	US-10-637-313-62	Sequence 62, Appl
33	660	98.5	644	5	US-10-637-313-64	Sequence 64, Appl
34	660	98.5	644	5	US-10-637-313-76	Sequence 76, Appl
35	660	98.5	644	5	US-10-741-600-1180	Sequence 1180, Ap
36	660	98.5	644	5	US-10-450-763-51460	Sequence 51460, A
37	656	97.9	644	5	US-10-637-313-66	Sequence 66, Appl
38	653	97.5	644	5	US-10-637-313-68	Sequence 68, Appl
39	653	97.5	644	5	US-10-637-313-70	Sequence 70, Appl
40	653	97.5	644	5	US-10-637-313-72	Sequence 72, Appl
41	648	96.7	644	5	US-10-637-313-74	Sequence 74, Appl
42	628	93.7	127	5	US-10-661-784-3	Sequence 3, Appl1
43	589.5	88.0	435	5	US-10-450-763-51464	Sequence 51464, A
44	554	82.7	357	5	US-10-637-313-10	Sequence 10, Appl
45	554	82.7	357	5	US-10-637-313-46	Sequence 46, Appl

ALIGNMENTS

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RESULT 1
US-10-661-784-2
; Sequence 2, Application US/10661784
; Publication No. US20050058599A1
; GENERAL INFORMATION:
; APPLICANT: MAZAR, Andrew
; TITLE OF INVENTION: Human Kininogen D3 Domain Polypeptide as an Anti-Angiogenic and
; FILE REFERENCE: 38342-193024
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/401,279
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-661-784-2

Query Match      100.0%; Score 670; DB 5; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e-63;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GSGKDFVQPTKICVGCPRDIPITNSPELEETLTHTTKLNENNATPFKIDNKKARVQ 60
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Db      1 GSGKDFVQPTKICVGCPRDIPITNSPELEETLTHTTKLNENNATPFKIDNKKARVQ 60

Cy      61 VVAKKTFIDVAETTESKESNELETSCETKLGSLDCAEVVYVPMKKIYPTVNC 120
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Db      61 VVAKKTFIDVAETTESKESNELETSCETKLGSLDCAEVVYVPMKKIYPTVNC 120

Cy      121 QPLGM 125
        |||
Db      121 QPLGM 125

RESULT 2
US-10-661-784-1
; Sequence 1, Application US/10661784
; Publication No. US20050058599A1
; GENERAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: MAZAR, Andrew
; TITLE OF INVENTION: Human Kininogen D3 Domain Polypeptide as an Anti-Angiogenic and
; FILE REFERENCE: 38342-193024
; CURRENT APPLICATION NUMBER: US/10/661,784

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;; CURRENT FILING DATE: 2003-09-15
;; PRIOR APPLICATION NUMBER: US 60/401,279
;; PRIOR FILING DATE: 2002-09-13
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 1
;; LENGTH: 123
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-661-784-1

Query Match 98.5%; Score 660; DB 5; Length 123;
Best Local Similarity 100.0%; Pred. No. 7,2e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 62
DB 1 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 60
QY 63 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 122
DB 61 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 120
QY 123 LGM 125
DB 121 LGM 123

RESULT 3
US-10-893-315-102
;; Sequence 102, Application US/10893315
;; Publication No. US20050147987A1
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.
;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
;; FILE REFERENCE: CLO00786
;; CURRENT APPLICATION NUMBER: US/10/893,315
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: 60/231,397
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 2172
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 102
;; LENGTH: 362
;; TYPE: PRT
;; ORGANISM: Human
US-10-893-315-102

Query Match 98.5%; Score 660; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2,9e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 62
DB 188 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 247
QY 63 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 122
DB 248 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 307
QY 123 LGM 125
DB 308 LGM 310

RESULT 4
US-10-893-315-104
;; Sequence 104, Application US/10893315
;; Publication No. US20050147987A1
;; GENERAL INFORMATION:
;; APPLICANT: VENTER, J. Craig et al.

;; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
;; FILE REFERENCE: CLO00786
;; CURRENT APPLICATION NUMBER: US/10/893,315
;; CURRENT FILING DATE: 2004-07-19
;; PRIOR APPLICATION NUMBER: 60/231,397
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 2172
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 362
;; TYPE: PRT
;; ORGANISM: Human
US-10-893-315-104

Query Match 98.5%; Score 660; DB 5; Length 362;
Best Local Similarity 100.0%; Pred. No. 2,9e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 62
DB 188 GKDVPPTKICVGCPRDIPNTPSPLEETLHTITKLNANNATYFKIDNVKARVQV 247
QY 63 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 122
DB 248 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYVPEKKIYPTVNCOP 307
QY 123 LGM 125
DB 308 LGM 310

RESULT 5
US-10-162-335-82
;; Sequence 82, Application US/10162335
;; Publication No. US2004009480A1
;; GENERAL INFORMATION:
;; APPLICANT: Anderson, David W.
;; APPLICANT: Baumgartner, Jason C.
;; APPLICANT: Boldog, Ferenc L.
;; APPLICANT: Caeman, Stacie J.
;; APPLICANT: Edinger, Shlomit R.
;; APPLICANT: Gangoli, Bha A.
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Gorman, Linda
;; APPLICANT: Guo, Xiaojia (Sasha)
;; APPLICANT: Hjalte, Tord
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Li, Li
;; APPLICANT: MacDougall, John R.
;; APPLICANT: Malysankar, Uriel M.
;; APPLICANT: Miller, Isabelle
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Patlurajan, Meera
;; APPLICANT: Pena, Carol E. A.
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Shinkets, Richard A.
;; APPLICANT: Stone, David J.
;; APPLICANT: Spytek, Kimberly A.
;; APPLICANT: Verne, Corine A. M.
;; APPLICANT: Voss, Edward Z.
;; APPLICANT: Zernusen, Bryan D.
;; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
;; FILE REFERENCE: 21402-377 B
;; CURRENT APPLICATION NUMBER: US/10/162,335
;; CURRENT FILING DATE: 2002-10-01
;; PRIOR APPLICATION NUMBER: 60/295,607
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/295,661
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/296,404
;; PRIOR FILING DATE: 2001-06-06

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;; PRIOR APPLICATION NUMBER: 60/296,418
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/297,414
;; PRIOR FILING DATE: 2001-06-11
;; PRIOR APPLICATION NUMBER: 60/297,567
;; PRIOR FILING DATE: 2001-06-12
;; PRIOR APPLICATION NUMBER: 60/298,285
;; PRIOR FILING DATE: 2001-06-14
;; PRIOR APPLICATION NUMBER: 60/298,556
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/299,949
;; PRIOR FILING DATE: 2001-06-21
;; PRIOR APPLICATION NUMBER: 60/300,883
;; PRIOR FILING DATE: 2001-06-26
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 201
;; SEQ ID NO: 82
;; LENGTH: 390
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-162-335-82.

Query Match          98.5%; Score 660; DB 4; Length 390;
Best Local Similarity 100.0%; Pred. No. 3,1e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPNPSPELEBTLTHITTKLNAENNATFYFKIDNVKKARQGV 62
DB 216 GKDFVQPTKICVGCPRDIPNPSPELEBTLTHITTKLNAENNATFYFKIDNVKKARQGV 275
QY 63 AGKRYFIDFVARETTCSKESNEBELTESCETKKLGOSLDCAAEVYVVPWEKKIYPTVNCOP 122
DB 276 AGKRYFIDFVARETTCSKESNEBELTESCETKKLGOSLDCAAEVYVVPWEKKIYPTVNCOP 335
QY 123 LGM 125
DB 336 LGM 338

RESULT 6
US-10-637-313-32
;; Sequence 32, Application US/10637313
;; Publication No. US2004022979A1
;; GENERAL INFORMATION:
;; APPLICANT: Ramesh Kekuda
;; APPLICANT: Uziel Malyankar
;; APPLICANT: David Anderson
;; APPLICANT: Saaba Guo
;; APPLICANT: Mel Zhong
;; APPLICANT: Muralidhara Padigaru
;; APPLICANT: Stacie Casman
;; APPLICANT: Ferenc Boldog
;; APPLICANT: Charles Miller
;; APPLICANT: Nikolai Khramtsov
;; APPLICANT: Corine Verneet
;; APPLICANT: Meera Patcurajan
;; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;; FILE REFERENCE: 21402-593B
;; CURRENT APPLICATION NUMBER: US/10/637,313
;; CURRENT FILING DATE: 2003-08-08
;; PRIOR APPLICATION NUMBER: 10/162335
;; PRIOR FILING DATE: 2002-06-03
;; PRIOR APPLICATION NUMBER: 60/295607
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/295661
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/296404
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/296418
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/298285
;; PRIOR FILING DATE: 2001-06-14
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;; PRIOR APPLICATION NUMBER: 60/298556
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/299949
;; PRIOR FILING DATE: 2001-06-21
;; PRIOR APPLICATION NUMBER: 60/300883
;; PRIOR FILING DATE: 2001-06-26
;; PRIOR APPLICATION NUMBER: 60/301550
;; PRIOR FILING DATE: 2001-06-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 255
;; SOFTWARE: CuroSeqList version 0.1
;; SEQ ID NO: 32
;; LENGTH: 390
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-637-313-32

Query Match          98.5%; Score 660; DB 5; Length 390;
Best Local Similarity 100.0%; Pred. No. 3,1e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPNPSPELEBTLTHITTKLNAENNATFYFKIDNVKKARQGV 62
DB 216 GKDFVQPTKICVGCPRDIPNPSPELEBTLTHITTKLNAENNATFYFKIDNVKKARQGV 275
QY 63 AGKRYFIDFVARETTCSKESNEBELTESCETKKLGOSLDCAAEVYVVPWEKKIYPTVNCOP 122
DB 276 AGKRYFIDFVARETTCSKESNEBELTESCETKKLGOSLDCAAEVYVVPWEKKIYPTVNCOP 335
QY 123 LGM 125
DB 336 LGM 338

RESULT 7
US-10-162-335-70
;; Sequence 70, Application US/10162335
;; Publication No. US20040009480A1
;; GENERAL INFORMATION:
;; APPLICANT: Anderson, David W.
;; APPLICANT: Baumgartner, Jason C.
;; APPLICANT: Boldog, Ferenc L.
;; APPLICANT: Casman, Stacie J.
;; APPLICANT: Edinger, Shlomit R.
;; APPLICANT: Gangoli, Esna A.
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Gorman, Linda
;; APPLICANT: Guo, Xiaojia (Saaba)
;; APPLICANT: Hjalte, Torild
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Li, Li
;; APPLICANT: MacDougall, John R.
;; APPLICANT: Malyankar, Uziel M.
;; APPLICANT: Miller, Isabelle
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Patcurajan, Meera
;; APPLICANT: Pena, Carol E. A.
;; APPLICANT: Rastelli, Luca
;; APPLICANT: Shinkets, Richard A.
;; APPLICANT: Stone, David J.
;; APPLICANT: Spytek, Kimberly A.
;; APPLICANT: Verneet, Corine A. M.
;; APPLICANT: Voss, Edward Z.
;; APPLICANT: Zehnusen, Bryan D.
;; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
;; FILE REFERENCE: 21402-377 B
;; CURRENT APPLICATION NUMBER: US/10/162,335
;; CURRENT FILING DATE: 2002-10-01
;; PRIOR APPLICATION NUMBER: 60/295,607
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/295,661
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: 60/296,404
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/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/296,418
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/297,414
/ PRIOR FILING DATE: 2001-06-11
/ PRIOR APPLICATION NUMBER: 60/297,567
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: 60/298,285
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/298,556
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/299,949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300,883
/ PRIOR FILING DATE: 2001-06-26
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 201
/ SEQ ID NO: 70
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-162-335-70

Query Match 98.5%; Score 660; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.2e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 62
DB 224 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 283
QY 63 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 122
DB 284 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 343

QY 123 LGM 125
DB 344 LGM 346

RESULT 8
US-10-637-313-20

/ Sequence 20, Application US/10637313
/ Publication No. US200402297979A1
/ GENERAL INFORMATION:
/ APPLICANT: Rameah Kekuda
/ APPLICANT: Uriel Malyankar
/ APPLICANT: Li Li
/ APPLICANT: David Anderson
/ APPLICANT: Sashu Guo
/ APPLICANT: Mei Zhong
/ APPLICANT: Muralidhara Padigaru
/ APPLICANT: Stacie Casman
/ APPLICANT: Ferenc Boldog
/ APPLICANT: Charles Miller
/ APPLICANT: Nikolai Khramtsov
/ APPLICANT: Corine Verneet
/ APPLICANT: Meera Patlurajan
/ TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
/ FILE REFERENCE: 21402-5938
/ CURRENT FILING DATE: 2003-08-08
/ PRIOR APPLICATION NUMBER: 10/162335
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/295607
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/295661
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/296404
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/296418
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/298285

/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/298556
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/299949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300883
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: 60/301550
/ PRIOR FILING DATE: 2001-06-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 255
/ SOFTWARE: Curaseqlist version 0.1
/ SEQ ID NO: 20
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-637-313-20

Query Match 98.5%; Score 660; DB 5; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.2e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 62
DB 224 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 283
QY 63 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 122
DB 284 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 343

QY 123 LGM 125
DB 344 LGM 346

RESULT 9
US-09-919-039-29

/ Sequence 29, Application US/09919039
/ Publication No. US20030108871A1
/ GENERAL INFORMATION:
/ APPLICANT: Kaser, Matthew R.
/ TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
/ FILE REFERENCE: PA-0035 US
/ CURRENT FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: 60/222,113
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 401
/ SOFTWARE: PERL Program
/ SEQ ID NO: 29
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
US-09-919-039-29

Query Match 98.5%; Score 660; DB 3; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 62
DB 253 GQDFVQPTKICVCGPRDIPNTSPLEETLTHTITKLAENNATYFKIDNVKARVQV 312
QY 63 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 122
DB 313 AGKXYFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVYPWEKKIYPTVNCOP 372

QY 123 LGM 125
DB 373 LGM 375

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RESULT 10
US-10-637-313-24
; Sequence 24, Application US/1063313
; Publication No. US2004022979A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Urtel Malpankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Saasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Perenc Boidog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khramtsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patnajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-5938
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: Curoseq1st version 0.1
; SEQ ID NO 24
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-24

Query Match          98.5%; Score 660; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNPSPELETLTHITTKLAENNAATFFPKIDNVKARQV 62
DB 253 GKDFVQPTKICVGCPRDIPNPSPELETLTHITTKLAENNAATFFPKIDNVKARQV 312
QY 63 AGKXFFIDFVARBETTCESNEBELTESCETKKGOSLDCAAEVYVVPWEKKIYPTVNCOP 122
DB 313 AGKXFFIDFVARBETTCESNEBELTESCETKKGOSLDCAAEVYVVPWEKKIYPTVNCOP 372
QY 123 LGM 125
DB 373 LGM 375
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RESULT 11
US-10-741-600-1179
; Sequence 1179, Application US/10741600
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; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARIGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1179
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1179

Query Match          98.5%; Score 660; DB 5; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.5e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNPSPELETLTHITTKLAENNAATFFPKIDNVKARQV 62
DB 253 GKDFVQPTKICVGCPRDIPNPSPELETLTHITTKLAENNAATFFPKIDNVKARQV 312
QY 63 AGKXFFIDFVARBETTCESNEBELTESCETKKGOSLDCAAEVYVVPWEKKIYPTVNCOP 122
DB 313 AGKXFFIDFVARBETTCESNEBELTESCETKKGOSLDCAAEVYVVPWEKKIYPTVNCOP 372
QY 123 LGM 125
DB 373 LGM 375
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RESULT 12
US-10-741-600-1181
; Sequence 1181, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARIGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1181
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1181
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```
RESULT 13
US-10-893-315-101
; Sequence 101, Application US/10893315
; Publication No. US20050147987A1
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-10-893-315-101
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Query Match          98.5%; Score 660; DB 5; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 62
   |||
Db 188 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 247
QY 63 AGKTYFIDVARETTCSKESNEELTESCETKKLGGSLDCNAEYVVVPWEKKIYPTVNCOP 122
   |||
Db 248 AGKTYFIDVARETTCSKESNEELTESCETKKLGGSLDCNAEYVVVPWEKKIYPTVNCOP 307
QY 123 LGM 125
   |||
Db 308 LGM 310
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RESULT 14
US-10-893-315-105
; Sequence 105, Application US/10893315
; Publication No. US20050147987A1
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH TYPE II DIABETES AND OBESITY, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00786
; CURRENT APPLICATION NUMBER: US/10/893,315
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: 60/231,397
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Human
US-10-893-315-105
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Query Match          98.5%; Score 660; DB 5; Length 579;
Best Local Similarity 100.0%; Pred. No. 5.2e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 62
   |||
Db 188 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 247
QY 63 AGKTYFIDVARETTCSKESNEELTESCETKKLGGSLDCNAEYVVVPWEKKIYPTVNCOP 122
   |||
Db 248 AGKTYFIDVARETTCSKESNEELTESCETKKLGGSLDCNAEYVVVPWEKKIYPTVNCOP 307
QY 123 LGM 125
   |||
Db 308 LGM 310
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RESULT 15

US-10-162-335-72

; Sequence 72, Application US/10162335

; Publication No. US20040009480A1

; GENERAL INFORMATION:

; APPLICANT: Anderson, David W.

; APPLICANT: Baumgartner, Jason C.

; APPLICANT: Boldog, Ferenc L.

; APPLICANT: Casman, Stracie J.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Gangoli, Sana A.

; APPLICANT: Gerlach, Valerie

; APPLICANT: Gorman, Linda

; APPLICANT: Guo, Xiaojia (Saasha)

; APPLICANT: Hjalte, Tord

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Li, Li

; APPLICANT: MacDougall, John R.

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Miller, Isabelle

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Patnrajan, Meera

; APPLICANT: Pena, Carol E. A.

; APPLICANT: Raestelli, Luca

; APPLICANT: Shinkets, Richard A.

; APPLICANT: Stone, David J.

; APPLICANT: Spytek, Kimberly A.

; APPLICANT: Vernet, Corine A. M.

; APPLICANT: Voss, Edward Z.

; APPLICANT: Zernusen, Bryan D.

; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method

; FILE REFERENCE: 21402-377 B

; CURRENT APPLICATION NUMBER: US/10/162,335

; CURRENT FILING DATE: 2002-10-01

; PRIOR APPLICATION NUMBER: 60/295,607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295,661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296,404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296,418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/297,414

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 60/297,567

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: 60/298,285

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298,556

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/299,949

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/300,883

; PRIOR FILING DATE: 2001-06-26

; Remaining Prior Application data removed - See file wrapper or PALM.

; NUMBER OF SEQ ID NOS: 201

; SEQ ID NO 72

; LENGTH: 615

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-162-335-72

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Query Match          98.5%; Score 660; DB 4; Length 615;
Best Local Similarity 100.0%; Pred. No. 5.6e-61;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 62
   |||
Db 224 GKDFOPTKICVCGPRDIPITNSPELEETLTHITTKLNAENNATFYFKIDNVKKAQVQV 283
QY 63 AGKTYFIDVARETTCSKESNEELTESCETKKLGGSLDCNAEYVVVPWEKKIYPTVNCOP 122
   |||
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Db 284 AGKVFIDFVARETTCSESNBELTESCETKKGQSLDONAEVVVVPWEKKIYPTVNCQP 343

OY 123 LGM 125

Db 344 LGM 346

Search completed: February 8, 2006, 03:21:54
Job time : 179 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:19:03 ; Search time 16 Seconds
(without alignments)
91.547 Million cell updates/sec

Title: US-10-661-784-2

Perfect score: 670

Sequence: 1 GSGKDFVGPFRKICVGCPRD.....YVPEWEKKIYPTVNCQPLGM 125

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/FCI_NEM_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US11_NEM_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEM_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US66_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	165.5	24.7	167	6	US-10-689-742-197 Sequence 197, App
2	136	20.3	148	6	US-10-967-093-8 Sequence 8, Appl
3	133.5	19.9	146	6	US-10-967-093-10 Sequence 10, Appl
4	130	19.4	140	6	US-10-967-093-6 Sequence 6, Appl
5	129.5	19.3	140	6	US-10-967-093-4 Sequence 4, Appl
6	129.5	19.3	382	5	US-09-978-360A-425 Sequence 425, App
7	127.5	19.0	146	6	US-10-982-545-4 Sequence 4, Appl
8	127.5	19.0	146	6	US-10-967-093-2 Sequence 2, Appl
9	110.5	16.5	97	6	US-10-821-234-1337 Sequence 1237, Ap
10	94.5	14.1	345	6	US-10-888-962-7 Sequence 7, Appl
11	91.5	13.7	352	6	US-10-888-962-8 Sequence 8, Appl
12	88.5	13.2	367	6	US-10-888-962-6 Sequence 6, Appl
13	82	12.2	758	6	US-10-467-962B-12 Sequence 12, Appl
14	74	11.0	138	7	US-11-137-445-37 Sequence 37, Appl
15	72	10.7	359	7	US-10-888-962-5 Sequence 5, Appl
16	69	10.3	1126	6	US-10-485-517-248 Sequence 248, App
17	67	10.0	734	7	US-11-169-041-223 Sequence 223, App
18	65	9.7	734	7	US-11-093-274-40 Sequence 40, Appl
19	65	9.7	1187	6	US-10-821-234-955 Sequence 955, App
20	63.5	9.5	162	7	US-11-215-658-8 Sequence 8, Appl
21	63.5	9.5	1597	6	US-10-877-346-41 Sequence 41, Appl
22	63.5	9.5	1641	6	US-10-877-346-40 Sequence 40, Appl
23	63	9.4	697	7	US-11-074-176-62 Sequence 62, App
24	62.5	9.3	449	7	US-11-169-041-138 Sequence 138, App
25	62	9.3	583	7	US-11-080-991-64 Sequence 64, Appl

26	62	9.3	1038	7	US-11-107-028-1 Sequence 1, Appl
27	61.5	9.2	384	7	US-11-075-351-12 Sequence 12, Appl
28	61.5	9.2	628	6	US-10-793-626-2844 Sequence 2844, Ap
29	61.5	9.2	1178	7	US-11-044-899-29 Sequence 29, Appl
30	61.5	9.2	1286	6	US-10-877-346-38 Sequence 38, Appl
31	61.5	9.2	2053	6	US-10-877-346-11 Sequence 11, Appl
32	61.5	9.2	2066	6	US-10-877-346-9 Sequence 9, Appl
33	61	9.1	227	6	US-10-485-517-210 Sequence 210, App
34	61	9.1	227	6	US-10-485-517-241 Sequence 241, App
35	61	9.1	1306	6	US-10-467-657-5406 Sequence 5406, Ap
36	60.5	9.0	334	7	US-11-016-564-1 Sequence 1, Appl
37	60.5	9.0	391	7	US-11-207-626A-30 Sequence 30, Appl
38	60.5	9.0	407	7	US-11-016-564-7 Sequence 7, Appl
39	60.5	9.0	263	7	US-11-183-136-2 Sequence 2, Appl
40	60	9.0	267	7	US-11-052-554A-300 Sequence 300, App
41	60	9.0	651	6	US-10-821-234-1666 Sequence 1666, Ap
42	59.5	8.9	193	5	US-09-978-360A-558 Sequence 558, App
43	59.5	8.9	481	6	US-10-995-561-959 Sequence 959, App
44	59	8.8	248	7	US-11-054-515-1386 Sequence 1386, Ap
45	59	8.8	932	7	US-11-057-058-59 Sequence 59, Appl

ALIGNMENTS

```
RESULT 1
US-10-689-742-197
; Sequence 197, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racle, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; PRIOR FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent version 3.2
; SEQ ID NO 197
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-197

Query Match      24.7% Score 165.5; DB 6; Length 167;
Best Local Similarity 32.5%; Pred. No. 1.6e-10;
Matches 37; Conservative 22; Mismatches 50; Indels 5; Gaps 3;

QY      11 TKICVGCPRDIPNPSPELEFTLTHITTKLAENNAATPFKIDNKKAAQVAVAGKKYID 70
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      54 SRVPGFPKTKTKTNDPGVLQARYSVEKFNCTNDMPLEKESRITRALVQIQIKLWLE 113
      |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      71 FVAHETTSKESNELETSC---TKKLGSLDCAEYVVPWEKKI-YPTVNC 120
      |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      114 VEIGRTTKKQHLRL-DDCDPQNHITLKQTLSCYSEVAVPMLQHFVPIVIRC 166
      |||||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 2
US-10-967-093-8
; Sequence 8, Application US/10967093
; Publication No. US20050267021A1
; GENERAL INFORMATION:
; APPLICANT: Schlemann, William P.
; TITLE OF INVENTION: Cystatin C as an Antagonist of TGF-B and Methods Related Thereto
; FILE REFERENCE: 2879-104
```


CREATIVITY: nullio bapleus

FILE REFERENCE: 821A

```
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1237
/ LENGTH: 97
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1237

Query Match          16.5%; Score 110.5; DB 6; Length 97;
Best Local Similarity 28.9%; Pred. No. 4.6e-05;
Matches 24; Conservative 19; Mismatches 35; Indels 5; Gaps 2;

Qy 32 LHTTTKLAENNATYFKIDNVKARVQVAGKTFIDFVARETTCSKESNEBELTSC- 90
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LDFAVEGVKASNDMYHSRALQVVARAKQIVAGVNYFLDELGRITCTK--TOPNIDNCP 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 91 --ETKKGSLDCNAEVVVPWE 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 FHDQPHLKKKAFCSFOIYAVPWQ 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-888-962-7
/ Sequence 7, Application US/10888962
/ Publication No. US2005026531A1
/ GENERAL INFORMATION:
/ APPLICANT: Saint Louis University
/ APPLICANT: Ray, Ranjit
/ APPLICANT: Yie-Hwa, Chang
/ APPLICANT: Basu, Arnab
/ APPLICANT: Basu, Arnab
/ TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
/ FILE REFERENCE: SLU 03-013 PCT
/ CURRENT APPLICATION NUMBER: US/10/888,962
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: 60/487,126
/ PRIOR FILING DATE: 2003-07-12
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 7
/ LENGTH: 345
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-888-962-7

Query Match          14.1%; Score 94.5; DB 6; Length 345;
Best Local Similarity 26.0%; Pred. No. 0.01;
Matches 25; Conservative 18; Mismatches 48; Indels 5; Gaps 3;

Qy 2 SGKDFVQPTKICVGCPRDIPITNSPELEBTLHTTTKLAENNATYFKIDNVKARVQV 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 STPDASADVRRKLCPRCPILIRFNDTNVHTVNTALAAFNQNGT-YFKLVEISRQ- 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 62 VAGKTFIDFVARETTCSKESNEBELTSCETKGLQ 97
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 PLFVSTLVEFVIAATDCTA---KEVDPKACNLLAE 224
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-888-962-8
/ Sequence 8, Application US/10888962
/ Publication No. US2005026531A1
/ GENERAL INFORMATION:
/ APPLICANT: Saint Louis University
/ APPLICANT: Ray, Ranjit
/ APPLICANT: Yie-Hwa, Chang
/ APPLICANT: Basu, Arnab
/ APPLICANT: Basu, Arnab
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/ TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
/ FILE REFERENCE: Growth
/ FILE REFERENCE: SLU 03-013 PCT
/ CURRENT APPLICATION NUMBER: US/10/888,962
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: 60/487,126
/ PRIOR FILING DATE: 2003-07-12
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-888-962-8

Query Match          13.7%; Score 91.5; DB 6; Length 352;
Best Local Similarity 27.1%; Pred. No. 0.02;
Matches 26; Conservative 17; Mismatches 48; Indels 5; Gaps 3;

Qy 2 SGKDFVQPTKICVGCPRDIPITNSPELEBTLHTTTKLAENNATYFKIDNVKARVQV 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 STPDASADVRRKLCPRCPILIRFNDTNVHTVNTALAAFNQNGT-YFKLVEISRQ- 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 62 VAGKTFIDFVARETTCSKESNEBELTSCETKGLQ 97
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 PFPVSTLVEFVIAATDCTA---TQAEVTDPAKCNLLAE 224
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-10-888-962-6
/ Sequence 6, Application US/10888962
/ Publication No. US2005026531A1
/ GENERAL INFORMATION:
/ APPLICANT: Saint Louis University
/ APPLICANT: Ray, Ranjit
/ APPLICANT: Yie-Hwa, Chang
/ APPLICANT: Basu, Arnab
/ APPLICANT: Basu, Arnab
/ TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
/ FILE REFERENCE: SLU 03-013 PCT
/ CURRENT APPLICATION NUMBER: US/10/888,962
/ CURRENT FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: 60/487,126
/ PRIOR FILING DATE: 2003-07-12
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 367
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-888-962-6

Query Match          13.2%; Score 88.5; DB 6; Length 367;
Best Local Similarity 26.1%; Pred. No. 0.048;
Matches 35; Conservative 22; Mismatches 56; Indels 21; Gaps 8;

Qy 2 SGKDFVQPTKICVGCPRDIPITNSPELEBTLHTTTKLAENNATYFKIDNVKARVQV 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 SSPDSADVRRKVCQCPPLIAPLNDTRVHAAFAAIAAFNAQNGS-NFQLEISRQ- 192
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 62 VAGKTFIDFVARETTCSKESNEBELTSCETKGLQ 108
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 LEPSTY-VFPTVSGTDCVAKENTAEAKCNLLAEKQYGFKATLSEKLG-----GAEVAVT 246
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 109 PWEKKIYPTVNCQP 122
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 247 CTVFQTOP-VTSQP 259
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RESULT 13
US-10-467-962B-12
/ Sequence 12, Application US/10467962B
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/ Publication No. US20050246784A1
/ GENERAL INFORMATION:
/ APPLICANT: Pilsch, Gunnar
/ APPLICANT: Blau, Astrid
/ APPLICANT: Daeschner, Klaus
/ APPLICANT: Klein, Mathieu
/ TITLE OF INVENTION: Identification of Herbicidally Active Substances
/ FILE REFERENCE: 2000 857
/ CURRENT APPLICATION NUMBER: US/10/467,962B
/ PRIOR FILING DATE: 2003-08-14
/ PRIOR APPLICATION NUMBER: PCT/EP02/01466
/ PRIOR FILING DATE: 2002-02-13
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: PatentIn Vers. 2.0
/ SEQ ID NO 12
/ LENGTH: 758
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-467-962B-12
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Query Match 12.2%; Score 82; DB 6; Length 758;

Best Local Similarity 23.5%; Pred. No. 0.57;

Matches 32; Conservative 23; Mismatches 47; Indels 34; Gaps 5;

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Oy 10 PTKICVCGPRDIPNTSPLEETLTHTTKLAENNAATFYFKI--DNVKKARQVAVGKK- 66
Db 132 PALACLALARE-----RPLELEMLSRDVEVLVENGKPLFKGPSLKRMSLYLNSGLQG 187
Oy 67 -----YFIDFVARETTCSSESNEELTESCETKKLQGSIDCNAY 105
Db 188 IGLMDMEKASTVDLMLRLILSYVDVVASSE--SKOHKKEIMSESVRSILSGI---AKM 241
Oy 106 YVVPWEKKIYPTVNOQ 121
Db 242 SLRPPESNVHDTMQNQ 257
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RESULT 14

US-11-137-465-37

/ Sequence 37, Application US/11137465

/ Publication No. US2005025558A1

/ GENERAL INFORMATION:

/ APPLICANT: Agarwal, Pankaj

/ APPLICANT: Murdoch, Paul R.

/ APPLICANT: Rizvi, Safia K.

/ APPLICANT: Smith, Randall, F.

/ APPLICANT: Xiang, Zhaoying

/ APPLICANT: Kadnick, Karen

/ TITLE OF INVENTION: NOVEL COMPOUNDS

/ FILE REFERENCE: GPS0018

/ CURRENT APPLICATION NUMBER: US/11/137,465

/ PRIOR FILING DATE: 2005-05-25

/ PRIOR APPLICATION NUMBER: US/10/239,663

/ PRIOR FILING DATE: 2002-09-24

/ PRIOR APPLICATION NUMBER: PCT/US01/09226

/ PRIOR FILING DATE: 2001-03-22

/ PRIOR APPLICATION NUMBER: 60/192,158

/ PRIOR FILING DATE: 2000-03-24

/ PRIOR APPLICATION NUMBER: 60/192,668

/ PRIOR FILING DATE: 2000-03-27

/ PRIOR APPLICATION NUMBER: 60/200,166

/ PRIOR FILING DATE: 2000-04-27

/ NUMBER OF SEQ ID NOS: 66

/ SOFTWARE: PatSeq for Windows Version 3.0

/ SEQ ID NO 37

/ LENGTH: 138

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-137-465-37

Query Match 11.0%; Score 74; DB 7; Length 138;

Best Local Similarity 24.5%; Pred. No. 0.47;

Matches 23; Conservative 20; Mismatches 47; Indels 4; Gaps 2;

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Oy 19 RDIPTNSPELEETLTHTTKLAENNAATFYKIDNV-KKARQVAVGKKYFIDFVARETT 77
Db 35 ODIPQNYVYVOQALMFANKEY---NKASFITSSALGKEYKLDSDLEYIEVXIARTI 91
Oy 78 CSKESNEELTESCETKKLQGSIDCNAYVVPWE 111
Db 92 CKKISDENCAFGQEDPPKQKQVVFCTFYASKPK 125
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RESULT 15

US-10-888-962-5

/ Sequence 5, Application US/10888962

/ Publication No. US20050266531A1

/ GENERAL INFORMATION:

/ APPLICANT: Saint Louis University

/ APPLICANT: Ray, Ranjit

/ APPLICANT: Yie-Hwa, Chang

/ APPLICANT: Ray, Ratna

/ APPLICANT: Basu, Arnab

/ TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell

/ FILE REFERENCE: SLU 03-013 PCT

/ CURRENT APPLICATION NUMBER: US/10/888,962

/ PRIOR FILING DATE: 2004-07-09

/ PRIOR APPLICATION NUMBER: 60/487,126

/ PRIOR FILING DATE: 2003-07-12

/ NUMBER OF SEQ ID NOS: 15

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 5

/ LENGTH: 359

/ TYPE: PRT

/ ORGANISM: Bos taurus

US-10-888-962-5

Query Match 10.7%; Score 72; DB 6; Length 359;

Best Local Similarity 22.8%; Pred. No. 2.5;

Matches 23; Conservative 16; Mismatches 48; Indels 14; Gaps 3;

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Oy 2 SGKDFVQPPYKICVCGPRDIPNTSPLEETLTHTTKLAENNAATFYKIDNVKKARQV 61
Db 134 SSPDASDVRKLCPCDPLADLNDSDRVVHVAVEVALATFNASNGS-YQLVEISRAQ--- 189
Oy 62 VAGKKYFIDFVARETTCSKESNEELTESCETKKLQGSIDCN 102
Db 190 -----FVPLPVSVSVEPAVAATD-CTAKEVVDPTKCN 220
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Search completed: February 8, 2006, 03:22:16

Job time : 17 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:13:07 ; Search time 41 Seconds
(without alignments)
293.344 Million cell updates/sec

Title: US-10-661-784-2

Perfect score: 670

Sequence: 1 GSGKDFVQNPPTKICVGCPRD.....YVPMWKIPIPTVNCQPLGM 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	660	98.5	427	1 KGHUL1	kininogen, LMW pre
2	660	98.5	427	1 KGHUL1	kininogen, LMW pre
3	477	71.2	436	1 KGBOL1	kininogen, LMW I P
4	477	71.2	621	1 KGBOL1	kininogen, LMW I P
5	450	67.2	434	1 KGBOL2	kininogen, LMW II
6	450	67.2	619	1 KGBOL2	kininogen, LMW II
7	426	63.6	433	2 A28055	K-kininogen, LMW I
8	426	63.6	639	2 A25486	kininogen, HMW I P
9	409	61.0	430	2 A23897	major acute phase
10	409	61.0	430	2 B28055	T-kininogen, LMW I
11	402	60.0	423	1 KGRM1	major acute phase
12	401	59.9	430	1 KGRM1	T-kininogen I prec
13	136	20.3	112	1 UD80	cyseratin - bovine
14	133	19.9	91	2 S68035	T-kininogen (clone
15	133	19.9	91	2 S68035	T-kininogen (clone
16	130	19.4	127	2 S07085	cyseratin C precurs
17	129	19.3	120	2 S10587	cyseratin C - rat
18	128	19.1	111	2 A28193	cyseratin - puff ad
19	127.5	19.0	140	2 A36163	cyseratin C precurs
20	127.5	19.0	146	1 UD80	cyseratin C precurs
21	125	18.7	141	2 B29632	cyseratin SA precur
22	118.5	17.7	139	1 UDCH	cyseratin precursor
23	113.5	16.9	122	2 A43644	barocystatin A pr
24	113	16.9	141	2 J01470	cyseratin S precurs
25	111.5	16.6	111	1 J02040	cyseratin - chum sa
26	109.5	16.3	141	1 UD80P2	cyseratin SN precur
27	109	16.0	141	1 UD80P1	cyseratin S precurs
28	107.5	16.0	132	2 J04918	cyseratin precursor
29	107	16.0	139	2 T33740	hypothetical prote

30	105.5	15.7	162	2 A43428	onchocystatin - ne
31	97.5	14.6	133	2 J04007	cyseratin II - maize
32	97	14.5	135	2 J04536	cyseratin precursor
33	95.5	14.3	143	2 T33301	hypothetical prote
34	95	14.2	142	2 A47142	cyseratin D precurs
35	94.5	14.1	145	2 S21094	alpha-2-HS-glycop
36	93.5	14.0	139	2 A45361	cyseratin-related e
37	92	13.7	100	2 JH0269	cyseratin - avocado
38	91.5	13.7	135	2 S27239	cyseratin proteins
39	91.5	13.7	125	2 A32827	fetuin precursor -
40	88.5	13.2	125	2 T00752	cyseratin proteins
41	88.5	13.2	134	2 J04882	cyseratin - maize
42	88.5	13.2	134	2 S54828	cysteine proteins
43	88.5	13.2	367	1 M0H1	alpha-2-HS-glycop
44	85	12.7	199	2 S65071	cyseratin - field m
45	84.5	12.6	592	2 T50516	Ca2+ dependent lip

ALIGNMENTS

RESULT 1
KGHUL1
kininogen, LMW precursor [validated] - human
N.Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N.Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C.Species: Homo sapiens (man)
C.Date: 06-Jul-1982 #sequence revision 27-Nov-1985 #text_change 09-Jul-2004
C.Accession: A01280; B25276; A27900; A27699; A31905; A34030
R.Ohkuho, I.; Kurachi, K.; Takasawa, T.; Shiohara, H.; Sasaki, M.
Biochemistry 23: 5691-5697, 1984
A.Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ident
A.Reference number: A90490; MUID:85122621; PMID:6441591
A.Accession: A01280
A.Molecule type: mRNA
A.Residues: 1-427 <OHK>
A.Cross-references: UNIPROT:P01042; UNIPARC:UPI000000029C; GB:K02566; NID:q177889; PIDN
R.Takagaki, Y.; Kitamura, N.; Nakamishi, S.
J. Biol. Chem. 260: 8601-8609, 1985
A.Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low
A.Reference number: A92544; MUID:85234582; PMID:2989293
A.Accession: B25276
A.Molecule type: mRNA
A.Residues: 1-427 <TAK>
A.Cross-references: UNIPARC:UPI000000029C; GB:M1437; NID:q186751; PIDN:AAB59551.1; PID
R.Votspetch, F.; Kellermann, J.; Henschen, A.; Raut, G.; Mueller-Eberhard, W.
in Kinins IV, part A, Greenbaum, L.M., and Margolis, H.S., eds., pp.91-95, Plenum, New
A.Title: Amino acid sequence of the light chain of human low molecular mass kininogen.
A.Reference number: A27900
A.Accession: A27900
A.Molecule type: protein
A.Residues: 390-427 <LOT>
A.Cross-references: UNIPARC:UPI00001742A0
R.Mindrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Secliff, A.G.
Biochem. Biophys. Res. Commun. 152: 519-526, 1988
A.Title: A new kinin moiety in human plasma kininogens.
A.Reference number: A27699; MUID:88209021; PMID:3365237
A.Accession: A27699
A.Molecule type: protein
A.Residues: 380-389 <MIN>
A.Cross-references: UNIPARC:UPI000002C0F8
R.Maeda, H.; Matsunura, Y.; Kato, H.
J. Biol. Chem. 263: 16051-16054, 1988
A.Title: Purification and identification of [hydoxyprolyl(3)]bradykinin in ascitic fluid
A.Reference number: A31905; MUID:89034061; PMID:3182782
A.Accession: A31905
A.Molecule type: protein
A.Residues: 381-389 <MA>
A.Cross-references: UNIPARC:UPI000002CF4A
R.Saeguchi, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150: 511-516, 1988
A.Title: Identification of [hydoxyprolyl(3)]-lysyl-bradykinin released from human plas
A.Reference number: A34030; MUID:88106632; PMID:3337729

A/Accession: A34030
 A/Molecule type: protein
 A/Residues: 380-389 <SAS>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Takagaki, Y.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A/Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight proteinase inhibitors
 A/Reference number: A92544; PMID:85234582; PMID:2989293
 A/Accession: A25276
 A/Molecule type: mRNA
 A/Residues: 1-592, 'I', 594-644 <TAK>
 A/Cross-references: UNIPARC:UPI000003JDSAC; GB:M1437; NID:q186751; PIDN:AA859550.1; PIDN:AA859550.1
 R/Huettner, E.A.; Roessler, D.; Mentle, R.; Asselstyn-Machleidt, I.
 FEBS Lett. 321, 93-97, 1993
 A/Title: Cloning, expression and characterization of human kininogen domain 3.
 A/Reference number: S32422; PMID:93223854; PMID:8467916
 A/Accession: S32422
 A/Molecule type: mRNA
 A/Residues: 'ANSM', 253-377 <AUE>
 A/Cross-references: UNIPARC:UPI0000174297
 A/Note: differences are due to known cloning artifacts
 R/Lottspeich, F.; Kellermann, J.; Henschen, A.; Foerster, B.; Muller-Berterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A/Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen.
 A/Reference number: A91153; PMID:86030270; PMID:4054110
 A/Accession: A91153
 A/Molecule type: protein
 A/Residues: 379-644 <LOT>
 A/Cross-references: UNIPARC:UPI0000174298
 A/Note: the bradykinin sequence preceding the light chain sequence was not determined in this clone
 R/Kellermann, J.; Lottspeich, F.; Henschen, A.; Muller-Berterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A/Title: Completion of the primary structure of human high-molecular-mass kininogen.
 A/Reference number: A24871; PMID:86108361; PMID:3484703
 A/Accession: A24871
 A/Molecule type: protein
 A/Residues: 'Z', 20-380 <KEL1>
 A/Cross-references: UNIPARC:UPI0000174299
 R/Kellermann, J.; Lottspeich, F.; Henschen, A.; Muller-Berterl, W.
 in Kinins IV. Greenbaum, L.M., and Margolis, H.S., ed., pp. 85-89, Plenum Press, New York, 1985
 A/Title: Amino acid sequence of the light chain of human high molecular mass kininogen.
 A/Reference number: A27899
 A/Accession: A27899
 A/Molecule type: protein
 A/Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
 A/Cross-references: UNIPARC:UPI0000174299
 R/Minamide, T.; Carretero, O.A.; Proud, D.; Walz, D.; Secliff, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A/Title: A new kinin moiety in human plasma kininogens.
 A/Reference number: A27699; PMID:88209021; PMID:3365237
 A/Accession: A27699
 A/Molecule type: protein
 A/Residues: 380-389 <MIN>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Maeda, H.; Matsumura, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A/Title: Purification and identification of [hydroxyprolyl(3)]-bradykinin in ascitic fluid
 A/Reference number: A31905; PMID:89034061; PMID:3182782
 A/Accession: A31905
 A/Molecule type: protein
 A/Residues: 381-389 <MAB>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Sasaquri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A/Title: Identification of [hydroxyprolyl(3)]-bradykinin released from human platelets
 A/Reference number: A34030; PMID:88106632; PMID:3337729
 A/Accession: A34030
 A/Molecule type: protein
 A/Residues: 380-389 <SAS>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Ikenari, B.; Gabrielic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A/Title: Human cathepsin B and cysteine proteinase inhibitors (CPis) in inflammatory an

A/Accession: A01279
 A/Molecule type: protein
 A/Residues: 380-389 <SAS>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Takagaki, Y.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 260, 8601-8609, 1985
 A/Title: Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight proteinase inhibitors
 A/Reference number: A92544; PMID:85234582; PMID:2989293
 A/Accession: A25276
 A/Molecule type: mRNA
 A/Residues: 1-592, 'I', 594-644 <TAK>
 A/Cross-references: UNIPARC:UPI000003JDSAC; GB:M1437; NID:q186751; PIDN:AA859550.1; PIDN:AA859550.1
 R/Huettner, E.A.; Roessler, D.; Mentle, R.; Asselstyn-Machleidt, I.
 FEBS Lett. 321, 93-97, 1993
 A/Title: Cloning, expression and characterization of human kininogen domain 3.
 A/Reference number: S32422; PMID:93223854; PMID:8467916
 A/Accession: S32422
 A/Molecule type: mRNA
 A/Residues: 'ANSM', 253-377 <AUE>
 A/Cross-references: UNIPARC:UPI0000174297
 A/Note: differences are due to known cloning artifacts
 R/Lottspeich, F.; Kellermann, J.; Henschen, A.; Foerster, B.; Muller-Berterl, W.
 Eur. J. Biochem. 152, 307-314, 1985
 A/Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen.
 A/Reference number: A91153; PMID:86030270; PMID:4054110
 A/Accession: A91153
 A/Molecule type: protein
 A/Residues: 379-644 <LOT>
 A/Cross-references: UNIPARC:UPI0000174298
 A/Note: the bradykinin sequence preceding the light chain sequence was not determined in this clone
 R/Kellermann, J.; Lottspeich, F.; Henschen, A.; Muller-Berterl, W.
 Eur. J. Biochem. 154, 471-478, 1986
 A/Title: Completion of the primary structure of human high-molecular-mass kininogen.
 A/Reference number: A24871; PMID:86108361; PMID:3484703
 A/Accession: A24871
 A/Molecule type: protein
 A/Residues: 'Z', 20-380 <KEL1>
 A/Cross-references: UNIPARC:UPI0000174299
 R/Kellermann, J.; Lottspeich, F.; Henschen, A.; Muller-Berterl, W.
 in Kinins IV. Greenbaum, L.M., and Margolis, H.S., ed., pp. 85-89, Plenum Press, New York, 1985
 A/Title: Amino acid sequence of the light chain of human high molecular mass kininogen.
 A/Reference number: A27899
 A/Accession: A27899
 A/Molecule type: protein
 A/Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
 A/Cross-references: UNIPARC:UPI0000174299
 R/Minamide, T.; Carretero, O.A.; Proud, D.; Walz, D.; Secliff, A.G.
 Biochem. Biophys. Res. Commun. 152, 519-526, 1988
 A/Title: A new kinin moiety in human plasma kininogens.
 A/Reference number: A27699; PMID:88209021; PMID:3365237
 A/Accession: A27699
 A/Molecule type: protein
 A/Residues: 380-389 <MIN>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Maeda, H.; Matsumura, Y.; Kato, H.
 J. Biol. Chem. 263, 16051-16054, 1988
 A/Title: Purification and identification of [hydroxyprolyl(3)]-bradykinin in ascitic fluid
 A/Reference number: A31905; PMID:89034061; PMID:3182782
 A/Accession: A31905
 A/Molecule type: protein
 A/Residues: 381-389 <MAB>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Sasaquri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
 Biochem. Biophys. Res. Commun. 150, 511-516, 1988
 A/Title: Identification of [hydroxyprolyl(3)]-bradykinin released from human platelets
 A/Reference number: A34030; PMID:88106632; PMID:3337729
 A/Accession: A34030
 A/Molecule type: protein
 A/Residues: 380-389 <SAS>
 A/Cross-references: UNIPARC:UPI000002C0F8
 R/Ikenari, B.; Gabrielic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, V.
 Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
 A/Title: Human cathepsin B and cysteine proteinase inhibitors (CPis) in inflammatory an

A:Accession: S02482
A:Molecule type: protein
A:Residues: 1-19,189-192,310-314,381-389 <LENI>
A:Cross-references: UNIPARC:UPI000002CP4A; UNIPARC:UPI000017429B
R:Kato, H./ Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A:Title: Isolation and identification of hydroxyproline analogues of bradykinin in human
A:Reference number: A61495; MUID:88211869; PMID:3366244
A:Accession: A61495
A:Molecule type: protein
A:Residues: 380-389 <KAT1>
A:Cross-references: UNIPARC:UPI000002C0F8
A:Experimental source: urine
A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
A:Accession: B61495
A:Molecule type: protein
A:Residues: 381-389 <KAT2>
A:Cross-references: UNIPARC:UPI000002CP4A
A:Experimental source: urine
A:Note: this peptide had Pro-383 modified to 4-hydroxyproline
A:Accession: C61495
A:Molecule type: protein
A:Residues: 380-389 <KAT3>
A:Cross-references: UNIPARC:UPI000002C0F8
R:Benaric, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.
FEBS Lett. 280, 211-215, 1991
A:Title: Inactivation of human cystatin C and kininogen by human cathepsin D.
A:Reference number: S14303; MUID:91192133; PMID:2013314
A:Accession: S14447
A:Molecule type: protein
A:Residues: 264-359, 'N', 361-375 <LENI2>
A:Cross-references: UNIPARC:UPI000017429D
R:Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A:Title: Human mast cell tryptase isoforms: separation and examination of substrate-specific
A:Reference number: S55239; MUID:95251593; PMID:7733867
A:Accession: S55239
A:Molecule type: protein
A:Residues: 450-452, 'X', 454, 'X', 456 <LIT>
A:Cross-references: UNIPARC:UPI000017429E
R:Stracek, J.; Machal, F.; le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nabec, P.; Belleville
FEBS Lett. 373, 207-211, 1995
A:Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like
A:Reference number: S68059; MUID:96033974; PMID:7589467
A:Accession: S68059
A:Molecule type: protein
A:Residues: 431-434 <STR>
A:Cross-references: UNIPARC:UPI000017429F
R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 260, 8610-8617, 1985
A:Title: Structural organization of the human kininogen gene and a model for its evolution
A:Reference number: A92545; MUID:85234583; PMID:2989294
A:Contents: annotation; gene organization
R:Pierce, J.V.
Fed. Proc. 27, 52-57, 1968
A:Title: Structural features of plasma kinins and kininogens.
A:Reference number: A91455; MUID:90255622; PMID:4952632
A:Contents: annotation; bradykinin
C:Comment: The HMW kininogen precursor and the LMW form are produced from the same gene
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of these
C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is im-
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, 1
C:Comment: The residue is present in the kininogen prior to the release of bradykinin.
A:Gene: GDB:KNG
A:Cross-references: GDB:125256; OMIM:228960
A:Map position: 3627-3q27
A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C:Superfamily: alternative; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupli-
F:1-18/Domain: signal sequence #status experimental <SIG>
F:19-644/Product: HMW kininogen I (prokinogen I) #status experimental <MAT1>
F:19-379,380-644/Product: HMW kininogen II #status experimental <MAT2>

[illegible]

C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-433/Product: R-kininogen, LWM I #status predicted <MAT>
 F:19-131/Domain: cystatin homology <CY1>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CY3>

Query Match 63.6%; Score 426; DB 2; Length 433;
 Best Local Similarity 65.0%; Pred. No. 1,2e-32;
 Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

QY 3 GDDFVQPTKICVCGCPDIPITNSPELEETLTHITTKLNNATPFYFKIDNVKKARQV 62
 DB 253 GDDLFELLPBDCGCCRNPVDSPELKEALGSHIAQLMNNHTTFYFKIDYKKAISQV 312
 QY 63 AGKVFIDFVARETTCKESNEELTESCETKKGSLDCAEYVYVWVEKKIYPTVNCOP 122
 DB 313 AGTKYVIEFTARETKCKESNAELTADCEKRLGSLNCNANVYMRPWEKVVPTVCKV 372
 QY 123 LGM 125
 DB 373 LDM 375

RESULT 8
 A25486
 A:kininogen, HMM I precursor - rat
 N:Contains: bradykinin
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
 C/Accession: A25486
 R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A>Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A:Reference number: A92625; PMID:87137443; PMID:3029068
 A:Accession: A25486
 A:Molecule type: mRNA
 A:Residues: 1-639 <KIT>
 A:Cross-references: UNIPROT:P08934; UNIPARC:UPI000012DF1B
 A/Note: the authors translated the codon CAA for residue 347 as Asn
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: alternative splicing
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-639/Product: kininogen, HMM I #status predicted <MAT>
 F:19-131/Domain: cystatin homology <CY1>
 F:142-253/Domain: cystatin homology <CY2>
 F:264-375/Domain: cystatin homology <CY3>

Query Match 63.6%; Score 426; DB 2; Length 639;
 Best Local Similarity 65.0%; Pred. No. 1.8e-32;
 Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

QY 3 GDDFVQPTKICVCGCPDIPITNSPELEETLTHITTKLNNATPFYFKIDNVKKARQV 62
 DB 253 GDDLFELLPBDCGCCRNPVDSPELKEALGSHIAQLMNNHTTFYFKIDYKKAISQV 312
 QY 63 AGKVFIDFVARETTCKESNEELTESCETKKGSLDCAEYVYVWVEKKIYPTVNCOP 122
 DB 313 AGTKYVIEFTARETKCKESNAELTADCEKRLGSLNCNANVYMRPWEKVVPTVCKV 372
 QY 123 LGM 125
 DB 373 LDM 375

RESULT 9
 A23897
 A:acute phase alpha-1 protein (version 2) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C/Accession: A23897; B23897
 R:Anderson, K.F.; Heath, E.C.

J. Biol. Chem. 260, 12065-12071, 1985
 A>Title: The relationship between rat major acute phase protein and the kininogens.
 A:Reference number: A23897; PMID:86008266; PMID:2413019
 A:Accession: A23897
 A:Molecule type: protein
 A:Residues: 1-14 <AND1>
 A:Cross-references: UNIPROT:P01048; UNIPARC:UPI0000177A63
 A:Accession: B23897
 A:Molecule type: mRNA
 A:Residues: 5-430 <AND2>
 A:Cross-references: UNIPARC:UPI0000170A0C; GB:M1661; NID:5205307; PIDN:AAA1570.1; PID
 A/Note: the authors translated the codon CTC for residue 410 as Arg, CTA for residue 415
 C:Superfamily: kininogen; cystatin homology
 F:19-130/Domain: cystatin homology <CY1>
 F:141-252/Domain: cystatin homology <CY2>
 F:263-374/Domain: cystatin homology <CY3>

Query Match 61.0%; Score 409; DB 2; Length 430;
 Best Local Similarity 61.8%; Pred. No. 4.7e-31;
 Matches 76; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 3 GDDFVQPTKICVCGCPDIPITNSPELEETLTHITTKLNNATPFYFKIDNVKKARQV 62
 DB 252 GDDLFSLPKKCFGCKNPVDSPELKEALGSHIAQLMNNHTTFYFKIDYKKAISQV 311
 QY 63 AGKVFIDFVARETTCKESNEELTESCETKKGSLDCAEYVYVWVEKKIYPTVNCOP 122
 DB 312 AGTKYVIEFTARETKCKESNAELTADCEKRLGSLNCNANVYMRPWEKVVPTVCKV 371
 QY 123 LGM 125
 DB 372 LDM 374

RESULT 10
 B28055
 T:kininogen, LWM II precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 09-Jul-2004
 C/Accession: B28055; E25486; B28526; C28526
 R:Funato-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.
 J. Biol. Chem. 260, 12054-12059, 1985
 A>Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and
 inhibitor.
 A:Reference number: A92496; PMID:86008264; PMID:2413018
 A:Accession: B28055
 A:Molecule type: mRNA
 A:Residues: 1-430 <FUR>
 A:Cross-references: UNIPROT:P08932; UNIPARC:UPI000012DF30
 R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A>Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A:Reference number: A92625; PMID:87137443; PMID:3029068
 A:Accession: E25486
 A:Molecule type: DNA
 A:Residues: 375-430 <KIT>
 A:Cross-references: UNIPARC:UPI0000003B0
 R:Biyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 973-979, 1988
 A>Title: Purification and characterization of rat T-kininogens isolated from plasma of
 A:Reference number: A92729; PMID:88087226; PMID:3121623
 A:Accession: B28526
 A:Molecule type: protein
 A:Residues: 'E', 20-25, 'MD', 28-48, 376-430 <ENJ>
 A:Cross-references: UNIPARC:UPI0000177A67
 A:Accession: C28526
 A:Molecule type: protein
 A:Residues: 'E', 20-48, 376-388, 'R', 390-419, 'ER', 422-430 <EN2>
 A:Cross-references: UNIPARC:UPI0000177A67
 C:Superfamily: kininogen; cystatin homology
 C:Keywords: glycoprotein; pyroglyutamic acid
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-430/Product: T-kininogen, LWM II #status experimental <MAT>

F/19-130/Domain: cystatin homology <CY1>
 F/141-252/Domain: cystatin homology <CY2>
 F/263-374/Domain: cystatin homology <CY3>
 F/19/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experiment
 F/62,126,168,204,362/Binding site: carboxylate (Asn) (covalent) #status predicted
 F/83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Diulfide bonds: #status

Query Match 61.0%; Score 409; DB 2; Length 430;
 Best Local Similarity 61.8%; Pred. No. 4,7e-31;
 Matches 76; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 3 GKDVPDPYKICVGCPRDIPITNSPELEETLTHITTKLAENNAFFYFKIDNVKKARQVY 62
 DB 252 GDDLFSLPKKCCGCPKGNIPVDSPELKEALGHSAQNAQHNLFFPKIDTVKKASQVY 311
 QY 63 AGKKYFIDFVARETTCKSKESNEELTESCEYTKLGGSIDCAEYVVPWEKKIYPTVNCOP 122
 DB 312 AGTKYVIEFVARETNSCKQNTTELTDCEYTKHGGSLNCANVYMPWENKVVPTVRCQA 371
 QY 123 LGM 125
 DB 372 LDM 374

RESULT 11
 KGRM
 Major acute phase alpha-1 protein precursor - rat (fragment)
 N/Contains: bradykinin
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 12-Apr-1996
 C/Accession: A01285
 R/Colo. T.; Ingilis, A.S.; Roxburgh, C.M.; Howlett, G.J.; Schreiber, G.
 P888 Lect. 182, 57-61, 1985
 A/Title: Major acute phase alpha-1-protein of the rat is homologous to bovine kininogen A
 A/Reference number: A01285; MID:85127561; PMID:2578992
 A/Accession: A01285
 A/Molecule type: mRNA
 A/Residues: 1-423 <COL>
 A/Cross-references: UNIPARC:UPI00001742A6
 C/Comment: This plasma glycoprotein inhibits cysteine proteinases. During acute inflammation.

C/Superfamily: kininogen; cystatin homology
 C/Keyword: bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein; inflam
 F/1-11/Domain: signal sequence (fragment) #status predicted <SIG>
 F/12-423/Product: major acute phase alpha-1 protein #status predicted <MAT>
 F/12-123/Domain: cystatin homology <CY1>
 F/134-245/Domain: cystatin homology <CY2>
 F/256-367/Domain: cystatin homology <CY3>
 F/171-379/Product: bradykinin #status predicted <BDY>
 F/12/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status predicted
 F/161,197/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 60.0%; Score 402; DB 1; Length 423;
 Best Local Similarity 61.8%; Pred. No. 2.1e-30;
 Matches 76; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 3 GKDVPDPYKICVGCPRDIPITNSPELEETLTHITTKLAENNAFFYFKIDNVKKARQVY 62
 DB 245 GDDLFSLPKKCCGCPKGNIPVDSPELKEALGHSAQNAQHNLFFPKIDTVKKASQVY 304
 QY 63 AGKKYFIDFVARETTCKSKESNEELTESCEYTKLGGSIDCAEYVVPWEKKIYPTVNCOP 122
 DB 305 AGTKYVIEFVARETNSCKQNTTELTDCEYTKHGGSLNCANVYMPWENKVVPTVRCQA 364
 QY 123 LGM 125
 DB 365 LDM 367

RESULT 12
 KGRM
 T-kininogen I precursor - rat
 N/Alternate names: 73K protein; LMW kininogen T-I

N/Contains: bradykinin; T-kinin
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 31-Dec-2004
 C/Accession: A01286; D25486; A28526; PLO193; J00027; B25488; A28525; S68036
 R/Furto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakaniishi, S.
 J. Biol. Chem. 260, 12054-12059, 1985
 A/Title: Primary structure of the mRNA encoding the rat precursors for bradykinin and
 inhibitor.
 A/Reference number: A92496; MID:86008264; PMID:2413018
 A/Accession: A01286
 A/Molecule type: mRNA
 A/Residues: 1-430 <FUR>
 A/Cross-references: UNIPROT:P01048; UNIPROT:Q63283; UNIPARC:UPI0000163B79; GB:M11883; N
 R.; Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakaniishi, S.
 J. Biol. Chem. 262, 2190-2198, 1987
 A/Title: Differing expression patterns and evolution of the rat kininogen gene family.
 A/Reference number: A92625; MID:87137443; PMID:3029068
 A/Accession: D25486
 A/Molecule type: DNA
 A/Residues: 375-430 <KIT>
 A/Cross-references: UNIPARC:UPI0000057F29
 R.; Enjoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 973-979, 1988
 A/Title: Purification and characterization of rat T-kininogens isolated from plasma of
 A/Reference number: A92729; MID:88087226; PMID:3121623
 A/Accession: A28526
 A/Molecule type: protein
 A/Residues: 'E', 20-48; 376-430 <ENJ>
 A/Cross-references: UNIPARC:UPI00001742A7; UNIPARC:UPI00001742A8
 R.; Kanda, S.; Sugiyama, K.; Takahashi, M.; Shumiyu, S.; Tomino, S.; Nagase, S.
 Jpn. J. Cancer Res. 81, 63-68, 1990
 A/Title: Identification of a protein increasing in serum of Nagase analbuminemic rats by
 A/Reference number: PLO193; MID:90216350; PMID:2108548
 A/Accession: PLO193
 A/Molecule type: mRNA
 A/Residues: 330-420, 'R', 422-429, 'P' <KAN>
 A/Cross-references: UNIPARC:UPI00001742A9
 R.; Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
 Gene 81, 119-128, 1989
 A/Title: Primary structure of a gene encoding rat T-kininogen.
 A/Reference number: J00027; MID:90034172; PMID:2806908
 A/Accession: J00027
 A/Molecule type: DNA
 A/Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258-31
 A/Cross-references: UNIPARC:UPI00001742A4
 A/Experimental source: strain Sprague-Dawley
 R.; Kageyama, R.; Kitamura, N.; Okubo, H.; Nakaniishi, S.
 J. Biol. Chem. 262, 2345-2351, 1987
 A/Title: Differing utilization of homologous transcription initiation sites of rat K and
 A/Reference number: A25488; MID:87137465; PMID:3818598
 A/Accession: B25488
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-48 <KAG>
 A/Cross-references: UNIPARC:UPI000000041B; GB:M14356; MID:g205090; PIDN:AAA41492.1; PID
 R.; Enjoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.
 J. Biol. Chem. 263, 965-972, 1988
 A/Title: Purification and characterization of two kinds of low molecular weight kininog
 A/Reference number: A28525; MID:88087225; PMID:3335530
 A/Accession: A28525
 A/Molecule type: protein
 A/Residues: 376-430 <EN2>
 A/Cross-references: UNIPARC:UPI00001742A8
 R.; Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.
 Arch. Biochem. Biophys. 322, 333-338, 1995
 A/Title: Identification of several isoforms of T-kininogen expressed in the liver of ag
 A/Reference number: S68034; MID:96032652; PMID:7574705
 A/Accession: S68036
 A/Molecule type: mRNA
 A/Residues: 340-430 <SIE>
 A/Cross-references: UNIPARC:UPI00001742A8
 A/Experimental source: clone PSG17
 C/Comment: At least three types of LMW kininogen precursors are present in rat plasma, t

ceding bradykinin.

C/Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after hydrolysis of an Arg or Lys, it is probably not released from its precursor by either tissue or plasma. C/Comment: The T-kininogens are produced in response to an inflammatory stimulant.

C/Genetics:

A/Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; 398/3

C/Superfamily: cystatin homology

C/Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein

F/1-10/Domain: signal sequence #status predicted <Sig>

F/19-430/Domain: cystatin homology <CY1>

F/141-252/Domain: cystatin homology <CY2>

F/263-374/Domain: cystatin homology <CY3>

F/378-386/Product: bradykinin #status predicted <BDY>

F/19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment

F/32,126,168,204,326/Binding site: carboxylate (Asn) (covalent) #status predicted

F/83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status

Query Match 59.9%; Score 401; DB 1; Length 430;

Best Local Similarity 61.8%; Pred. No. 2,7e-30;

Matches 76; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

QY 3 GKDVPPTKICVGCPRDIPNTSPLEETLTHTTKLAENNAFTFKIDNVKKARVQV 62

DB 252 GDDLFEILPKNCRGCPREIPVDSPELKEALGHSIAQLNQHNIIFYFKIDTVKKSQV 311

QY 63 AGKVFIDFVARETTSKESNEELTESCEFTKIGQSLDCAEYVVPWEKKIYPTVNCOP 122

DB 312 AGIYVIEFTARBTCSKOSTELTADCEFTKHLGQSLNCANVYMRPKNKVPVTRCOA 371

QY 123 LGM 125

DB 372 LDM 374

*RESULT 13

UDBO

Cystatin - bovine

N/Alternate names: chiol proteinase inhibitor

C/Species: Bos primigenius taurus (cattle)

C/Date: 28-Feb-1986 #sequence_revision 28-Feb-1986 #text_change 06-Dec-1996

C/Accession: A01271

R/Hirado, M.; Tsunawasa, S.; Sakiyama, F.; Minobe, M.; Fujii, S.

FEBS Lett. 186, 41-45, 1985

A/Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase in

A/Reference number: A01271; PMID:85231205; PMID:3851407

A/Accession: A01271

A/Residues: 1-112 <HIR>

A/Molecule type: protein

A/Cross-references: UNIPARC:UPI0000173259

C/Superfamily: cystatin; cysteine proteinase inhibitor

C/Keywords: colostrum; cysteine proteinase inhibitor

F/2-112/Domain: cystatin homology <CY3>

F/48-52/Region: inhibitory #status predicted

F/66-76,90-110/Disulfide bonds: #status predicted

Query Match 20.3%; Score 136; DB 1; Length 112;

Best Local Similarity 30.6%; Pred. No. 7.7e-05;

Matches 34; Conservative 22; Mismatches 31; Indels 24; Gaps 5;

QY 24 NSPELEETLTHTTKLAENNAFTFKIDNVKKARVQVAGKVFIDFVARETTSKESN 83

DB 12 NEEGVQALFPAVSEFNRKSRNDAYQSVVRVRRKQVVGSMVFLDVELGRITCTK--S 69

QY 84 BELTESC-----ETKLGQSLDCAEYVVPWEKKIYPTVNCOP 121

DB 70 QANLDSCPFNQPHLKREKL-----CSFOYVVPVPMN-----TINLVKFSQ 111

RESULT 14

S68035

T-kininogen (clone pSG17) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 31-Dec-2004

C/Accession: S68035

R/Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.

Arch. Biochem. Biophys. 322, 333-338, 1995

A/Title: Identification of several isoforms of T-kininogen expressed in the liver of ag

A/Reference number: S68034; PMID:96032652; PMID:7574705

A/Accession: S68035

A/Molecule type: mRNA

A/Residues: 1-91 <STE>

A/Cross-references: UNIPROT:P70517; UNIPROT:Q63581; UNIPARC:UPI0000177A60

A/Experimental source: liver

C/Superfamily: cystatin homology

C/Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

Query Match 19.9%; Score 133; DB 2; Length 91;

Best Local Similarity 68.6%; Pred. No. 1.2e-05;

Matches 24; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 91 ETKLGQSLDCAEYVVPWEKKIYPTVNCOP 125

DB 1 ETKHLGQSLNCANVYMRPKNKVPVTRCOALDM 35

RESULT 15

S68034

T-kininogen (clone pSG22) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 31-Dec-2004

C/Accession: S68034

R/Sierra, F.; Walter, R.; Vautravers, P.; Guigoz, Y.

Arch. Biochem. Biophys. 322, 333-338, 1995

A/Title: Identification of several isoforms of T-kininogen expressed in the liver of ag

A/Reference number: S68034; PMID:96032652; PMID:7574705

A/Accession: S68034

A/Molecule type: mRNA

A/Residues: 1-91 <STE>

A/Cross-references: UNIPROT:P70517; UNIPROT:Q63581; UNIPARC:UPI0000177A5F

A/Experimental source: liver

C/Superfamily: cystatin homology

C/Keywords: alternative splicing; cysteine proteinase inhibitor; plasma

Query Match 19.9%; Score 133; DB 2; Length 91;

Best Local Similarity 68.6%; Pred. No. 1.2e-05;

Matches 24; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 91 ETKLGQSLDCAEYVVPWEKKIYPTVNCOP 125

DB 1 ETKHLGQSLNCANVYMRPKNKVPVTRCOALDM 35

Search completed: February 8, 2006, 03:17:56

Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 8, 2006, 03:09:37 ; Search time 252 Seconds

(Without alignments)
349.964 Million cell updates/sec

Title: US-10-661-784-2

Perfect score: 670

Sequence: 1 GSGKDFVQPTKICVGCPRD.....YVWPWKIYPTVNCQPLGM 125

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	660	98.5	427	Q53EQ0_HUMAN	Q53EQ0 homo sapien
2	660	98.5	427	Q6PAU9_HUMAN	Q6PAU9 homo sapien
3	660	98.5	644	KNK1_HUMAN	P01042 homo sapien
4	477	71.2	621	KNK1_BOVIN	P01044 bos taurus
5	450	67.2	619	KNK2_BOVIN	P01045 bos taurus
6	434	64.8	480	Q6S911_MOUSE	Q6S911 mus musculus
7	434	64.8	661	Q6S911_MOUSE	Q6S911 mus musculus
8	426	63.6	433	Q5M8A0_RAT	Q5M8A0 rattus norv
9	426	63.6	433	KNK1_RAT	P08934 rattus norv
10	425	63.4	433	Q6S910_MOUSE	Q6S910 mus musculus
11	425	63.4	462	Q6S912_MOUSE	Q6S912 mus musculus
12	425	63.4	644	Q6S913_MOUSE	Q6S913 mus musculus
13	409	61.0	430	KNK2_RAT	P08932 rattus norv
14	409	61.0	430	Q5M894_RAT	Q5M894 rattus norv
15	404	60.3	140	Q7YRP6_PIG	Q7YRP6 sus scrofa
16	401	59.9	430	KNK1_RAT	P01048 rattus norv
17	401	59.9	430	Q5P0U1_RAT	Q5P0U1 rattus norv
18	399	59.6	430	Q63581_RAT	Q63581 rattus norv
19	364	54.3	634	Q6DMP4_MOUSE	Q6DMP4 mus musculus
20	176	26.3	335	Q4STD5_TETNG	Q4STD5 tetraodon n
21	175	26.1	144	CYTP_MOUSE	Q89038 mus musculus
22	175	26.1	167	Q9QWU5_MOUSE	Q9QWU5 mus musculus
23	173	25.8	332	CYTP_HUMAN	Q76096 homo sapien
24	165.5	24.7	145	Q5H2U6_XENTR	Q5H2U6 xenopus tiro
25	165.5	24.6	331	Q6FJ95_HUMAN	Q6FJ95 homo sapien
26	165	23.4	146	Q5XJ76_BRARE	Q5XJ76 brachydanio
27	156.5	23.2	146	Q5M8F3_XENTR	Q5M8F3 xenopus tiro
28	155.5	22.8	138	Q4SZM6_TETNG	Q4SZM6 tetraodon n
29	152.5	22.8	462	Q7SYH2_XENLA	Q7SYH2 xenopus lae
30	152.5	22.8	462	Q7ZY91_XENLA	Q7ZY91 xenopus lae
31	152.5	22.8	465	Q801E5_XENLA	Q801E5 xenopus lae

32	152.5	22.8	586	2	Q5XKA7_XENLA	Q5XKA7 xenopus lae
33	148.5	22.2	318	2	Q4SMW7_TETNG	Q4SMW7 tetraodon n
34	138.5	20.7	149	1	CYTM_HUMAN	Q15828 homo sapien
35	138.5	20.7	149	2	Q6IBD2_HUMAN	Q6IBD2 homo sapien
36	138.5	20.7	149	2	Q540N7_HUMAN	Q540N7 homo sapien
37	136	20.3	148	1	CYTC_BOVIN	P01035 bos taurus
38	136	20.3	148	1	Q54A26_BOVIN	Q54A26 bos taurus
39	133.5	19.9	146	1	CYTC_MACMU	Q19092 macaca mula
40	132.5	19.8	146	1	CYTC_SALSC	Q19093 saimiri bcl
41	131	19.6	140	2	Q6T6T4_XENTR	Q6T6T4 bclis gadon
42	131	19.6	454	2	Q66L07_XENLA	Q66L07 xenopus lae
43	130	19.4	127	1	CYTC_RAT	P14841 rattus norv
44	130	19.4	140	2	Q5M968_RAT	Q5M968 rattus norv
45	129.5	19.3	140	1	CYTC_MOUSE	P21460 mus musculus

ALIGNMENTS

RESULT 1	Q53EQ0_HUMAN PRELIMINARY; PRT; 427 AA.
ID	Q53EQ0_HUMAN PRELIMINARY; PRT; 427 AA.
AC	Q53EQ0;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Kininogen 1 variant (Fragment).
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Kidney;
RA	Maryama K., Sugano S.;
RT	"Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides.";
RL	Gene 138:171-174 (1994).
RN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Kidney;
RA	Suzuki Y., Yoshitomo K., Maryama K., Suyama A., Sugano S.;
RT	"Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";
RL	Gene 200:149-156 (1997).
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Kidney;
RA	Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL	Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AK223589; BAD97309.1; -; mRNA.
FT	NON TER
SO	SEQUENCE 427 AA; 47853 MW; C8BSA5F00BDBB9 CRC64;
Query Match	98.5%; Score 660; DB 2; Length 427;
Best Local Similarity	100.0%; Pred. No. 2.2e-53;
Matches 123; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	3 GKKFVPPFKICVGCPRDIPNTPSPELETLTHTTKANENNATFFKIDNVKARQVQV 62
Db	253 GKKFVPPFKICVGCPRDIPNTPSPELETLTHTTKANENNATFFKIDNVKARQVQV 312
Qy	63 AGKKYIDFVARETTSSKESNEELTSCETKKGGLDCAEYVVPWKIYPTVNCOP 122
Db	313 AGKKYIDFVARETTSSKESNEELTSCETKKGGLDCAEYVVPWKIYPTVNCOP 372
Qy	123 LGM 125
Db	373 LGM 375
RESULT 2	

06PAU9 HUMAN
ID 06PAU9 HUMAN PRELIMINARY; PRT; 427 AA.
AC 06PAU9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Kininogen 1.
GN Name=KNG1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tomihyaki S., Carninci P., Pizange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
*RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RX Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060039; AAH60039.1; -; mRNA.
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR InterPro; IPR000010; Prot_inh_cystac.
DR Pfam; PF00031; Cystecatin; 3.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSSTATIN; 2.
DR SEQUENCE 427 AA; 47901 MW; 17DB6C2346D75912 CRC64;
Query Match 98.5%; Score 660; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 2,2e-53;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GKDFVOPPTKICVGCPRDIPNPSLEETLTHITTKLAENNAATFYFKIDNVKKARVQV 62
DB 253 GKDFVOPPTKICVGCPRDIPNPSLEETLTHITTKLAENNAATFYFKIDNVKKARVQV 312
QY 63 AGKXYTFIDFVARETTCKESNEBELTESCTKKLGQSLDCNAVYVVPWEKKIYPTVNCOP 122
DB 313 AGKXYTFIDFVARETTCKESNEBELTESCTKKLGQSLDCNAVYVVPWEKKIYPTVNCOP 372
QY 123 LGM 125
DB 373 LGM 375

DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kininogen-1 precursor (Alpha-2-thiol proteinase inhibitor) [Contains:
DE Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-bradykinin
DE (Kallidin II); Kininogen-1 light chain; Low molecular weight growth
DE promoting factor].
GN Name=KNG1; Synonyms=BK, KNG;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM LMW).
RX MEDLINE=85122621; PubMed=6441591;
RA Ohkubo I., Kurachi K., Takasawa T., Shiohara H., Sasaki M.;
RT "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and
RT its identity with low molecular weight kininogen.";
RL Biochemistry 23:5691-5697(1984).
RN [2]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA) (ISOFORMS HMW AND LMW).
RC TISSUE=Liver;
RX MEDLINE=85234582; PubMed=2989293;
RA Takagaki Y., Kitamura N., Nakamichi S.;
RT "Cloning and sequence analysis of cDNAs for human high molecular
RT weight and low molecular weight prekallinogens. Primary structures of
RT two human prekallinogens.";
RL J. Biol. Chem. 260:8601-8609(1985).
RN [3]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA), AND VARIANTS SER-163; THR-178 AND
RP PRO-212.
RA Rieder M.J., de Ponte S.H., Kuidanek S.A., Rajkumar N., Smith J.D.,
RA Roth E.J., Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
RT PHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PROTEIN SEQUENCE OF 379-644.
RX MEDLINE=86030270; PubMed=4054110;
RA Lottspeich F., Kellermann J., Henschen A., Foerbach B.,
RA Mueller-Esterl W.;
RT "The amino acid sequence of the light chain of human high-molecular-
RT mass kininogen.";
RL Eur. J. Biochem. 152:307-314(1985).
RN [5]
RP PROTEIN SEQUENCE OF 381-389.
RX MEDLINE=90255622; PubMed=4952632;
RA Pierce J.V.;
RT "Structural features of plasma kinins and kininogens.";
RL Fed. Proc. 27:52-57(1968).
RN [6]
RP PROTEIN SEQUENCE OF 19-380, CARBOHYDRATE-LINKAGE SITES ASN-169 AND
RP ASN-205, AND ABSENCE OF CARBOHYDRATE AT ASN-48.
RX MEDLINE=6108361; PubMed=3484703;
RA Kellermann J., Lottspeich F., Henschen A., Muller-Esterl W.;
RT "Completion of the primary structure of human high-molecular-mass
RT kininogen. The amino acid sequence of the entire heavy chain and
RT evidence for its evolution by gene triplication.";
RL Eur. J. Biochem. 154:471-478(1986).
RN [7]
RP PROTEIN SEQUENCE OF 380-389, AND HYDROXYLATION SITE PRO-383.
RX MEDLINE=88211869; PubMed=336244; DOI=10.1016/0014-5793(88)80427-7;
RA Kato H., Matsumura Y., Maeda H.;
RT "Isolation and identification of hydroxyproline analogues of
RT bradykinin in human urine.";
RL FEBS Lett. 232:252-254(1988).
RN [8]
RP PROTEIN SEQUENCE OF 431-434, AND MASS SPECTROMETRY.
RX MEDLINE=96033974; PubMed=7589467; DOI=10.1016/0014-5793(95)01037-F;
RA Straczek J., Maschi F., Le Nguyen D., Becchi M., Heulin M.H.,
RA Nabet P., Belleville F.;
RT "Purification from human plasma of a tetrapeptide that potentiates
RT insulin-like growth factor-I activity in chick embryo cartilage.";
RL FEBS Lett. 373:207-211(1995).

RN [9]
 RP GENE STRUCTURE:
 RX MEDLINE=85334583; PubMed=2989294;
 RA Kitemura N., Kitegawa H., Fukushima D., Takagaki Y., Miyata T.,
 RT "Structural organization of the human kininogen gene and a model for
 RL its evolution.";
 RL J. Biol. Chem. 260:8610-8617(1985).
 RN [10]
 RP DISULFIDE BONDS.
 RA Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
 RT "Disulfide bonds in bovine HMW kininogens.";
 RL Seikagaku 56:808-808(1984).
 RN [11]
 RP AMINO-ACID COMPOSITION OF 381-389, AND HYDROXYLATION SITE PRO-383.
 RX MEDLINE=89034061; PubMed=3182782;
 RA Maeda H., Matsumura Y., Kato H.;
 RT "Purification and identification of [hydroxyprolyl3]bradykinin in
 RL ascitic fluid from a patient with gastric cancer.";
 RL J. Biol. Chem. 263:16051-16054(1988).
 RN [12]
 RP CARBOHYDRATE-LINKAGE SITE ASN-294.
 RX MEDLINE=22660472; PubMed=1275519; DOI=10.1038/nbt827;
 RA Zhang H., Li X.-J., Martin D.B., Aebbers R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RL hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 RN [13]
 RP CARBOHYDRATE-LINKAGE SITES ASN-169 AND ASN-294, AND MASS SPECTROMETRY.
 RX PubMed=14760718; DOI=10.1002/emc.200300556;
 RA Bunkenborg J., Plich B.J., Podelsnik A.V., Wisniewski J.R.;
 RT "Screening for N-glycosylated proteins by liquid chromatography mass
 RL spectrometry.";
 RL Proteomics 4:454-465(2004).
 RN [14]
 RP FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
 RC HMW-kininogen plays an important role in blood coagulation by
 RD helping to position optimally prekallikrein and factor XI next to
 RE factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
 RF induced aggregation of thrombocytes; (4) the active peptide
 RG bradykinin that is released from HMW-kininogen shows a variety of
 RH physiological effects; (4A) influence in smooth muscle
 RI contraction, (4B) induction of hypotension, (4C) natriuresis and
 RJ diuresis, (4D) decrease in blood glucose level, (4E) it is a
 RK mediator of inflammation and causes (4E1) increase in vascular
 RL permeability, (4E2) stimulation of nociceptors (4E3) release of
 RC other mediators of inflammation (e.g. prostaglandins), (4F) it has
 RD a cardioprotective effect (directly via bradykinin action, indirectly
 RE via endothelium-derived relaxing factor action); (5)
 RF LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
 RG kininogen is in contrast to HMW-kininogen not involved in blood
 RH clotting.
 RI
 RJ
 RK
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 RM
 RN
 RP
 RS
 RT
 RU
 RV
 RW
 RX
 RY
 RZ
 RA
 RB
 RC
 RD
 RE
 RF
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 RJ
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 RU
 RV
 RW
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 RY
 RZ
 RA
 RB
 RC
 RD
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 RF
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 RJ
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 RF
 RG
 RH
 RI
 RJ
 RK
 RL
 RM
 RN
 RP
 RS
 RT
 RU
 RV
 RW
 RX
 RY

	EMBL	M11521	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11522	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11523	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11524	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11525	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11526	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11527	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11528	AAB59550.1	JOINED	Genomic DNA.
DR	EMBL	M11437	AAB59551.1	- ; Genomic DNA.	
DR	EMBL	M11521	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11522	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11523	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11524	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11525	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11526	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11527	AAB59551.1	JOINED	Genomic DNA.
DR	EMBL	M11528	AAB59551.1	JOINED	Genomic DNA.
DR	PIR	A01279	KGHUHL	- ; Genomic DNA.	
DR	PIR	A01280	KGHUHL	- ; Genomic DNA.	
DR	SWISS-2DPAGE	P01042	HUMAN.		
DR	Ensembl	ENSG00000113889	Homo sapiens.		
DR	HGNC	HGNC:6383	KNG1.		
DR	Reactome	P01042	- ;		
DR	MIM	228960	- ;		
DR	GO	GO:0005576	C:extracellular region; NAS.		
DR	GO	GO:0008201	F:heparin binding; NAS.		
DR	GO	GO:0005102	F:receptor binding; IPT.		
DR	GO	GO:0008270	F:zinc ion binding; NAS.		
DR	GO	GO:0030146	P:dilutesis; TAS.		
DR	GO	GO:0006954	P:inflammatory response; TAS.		
DR	GO	GO:0030147	P:natriuresis; TAS.		
DR	GO	GO:0030195	P:negative regulation of blood coagulation; IDA.		
DR	GO	GO:0007185	P:negative regulation of cell adhesion; IDA.		
DR	GO	GO:0043065	P:positive regulation of apoptosis; NAS.		
DR	InterPro	IPRO02395	Kinogenen.		
DR	InterPro	IPRO00010	Prot inh_cystat.		
DR	Pfam	PF00031	Cysteatin; 3.		
DR	PRINTS	PRO0334	KINNOGEN.		
DR	SMART	SMO0043	CY; 3.		
DR	PROSITE	PS00287	CYSTATIN; 2.		
KW			Alternative splicing; Blood coagulation; Bradykinin;		
KW			Direct protein sequencing; Glycoprotein; Hydroxylation;		
KW			Inflammatory response; Plasma; Polymorphism; Protease inhibitor;		
KW			Pyroldione carboxylic acid; Repeat; Signal; Thiol protease inhibitor;		
KW			Vasodilative; Vasodilator.		
FT	SIGNAL	1	18		
FT	CHAIN	19	644	Kinogenen-1.	
Query Match		98.5%	Score 660; DB 1; Length 644;		
Best Local Similarity		100.0%	Pred. No. 3.4e-53;		
Matches 123;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;		
QY	3	GKDFVGPPTIKCVGCPRDIPFNSPELEETLTHITTKLMENNATFFFKIDNVKKAROVV	62		
Db	253	GKDFVGPPTIKCVGCPRDIPFNSPELEETLTHITTKLMENNATFFFKIDNVKKAROVV	312		
QY	63	AGKKYFDFAARETTCKESNEELTBSCEYTKLGOSLDCAEYVVYPWEKKIYPTVNCP	122		
Db	313	AGKKYFDFAARETTCKESNEELTBSCEYTKLGOSLDCAEYVVYPWEKKIYPTVNCP	372		
QY	123	LGM 125			
Db	373	LGM 375			
RESULT 4					
KNG1_BOVIN					
ID_KNG1_BOVIN	STANDARD;	PRT;	621 AA.		
AC	P01046; P01046;				
CT	21-JUL-1986 (Rel. 01, Created)				

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 46, Last annotation update)
DE Kininogen-1 precursor (Kininogen I) (Thiol proteinase inhibitor)
DE [Contains: Kininogen-1 heavy chain; Bradykinin (Kallidin I); Lysyl-
DE bradykinin (Kallidin II); Kininogen-1 light chain].
GN BOB (Bovine).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM HMW).
RP MEDLINE=84014106; PubMed=6571699;
RX Kltamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
RA "A single gene for bovine high molecular weight and low molecular
RT weight kininogens.";
RL Nature 305:545-549 (1983).
RN [2]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RP MEDLINE=83117859; PubMed=6572010;
RX Nawa H., Kltamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
RA "Primary structures of bovine liver low molecular weight kininogen
RT precursors and their two mRNAs.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).
RN [3]
RN PROTEIN SEQUENCE OF 19-378, AND CARBOHYDRATE-LINKAGE SITES ASN-87;
RP ASN-168; ASN-169; ASN-197 AND ASN-204.
RX MEDLINE=87137530; PubMed=3546295;
RA Suegoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,
RA Miyata T., Iwanaga S.;
RT "Bovine high molecular weight kininogen. The amino acid sequence,
RT positions of carbohydrate chains and disulfide bridges in the heavy
RL chain portion.";
RL J. Biol. Chem. 262:2768-2779 (1987).
RN [4]
RN PROTEIN SEQUENCE OF 378-393.
RX MEDLINE=70180420; PubMed=4986212;
RA Kato H., Nagasawa S., Suzuki T.;
RT "Studies on the structure of bovine kininogen: cleavages of disulfide
RL bonds and of methionyl bonds in kininogen-II.";
RL J. Biochem. 67:313-323 (1970).
RN [5]
RN PROTEIN SEQUENCE OF 458-498.
RX MEDLINE=75170265; PubMed=1169237;
RA Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
RT "Studies on the primary structure of bovine high-molecular-weight
RT kininogen. Amino acid sequence of a fragment ('histidine-rich
RT peptide') released by plasma kallikrein.";
RL J. Biochem. 77:55-68 (1975).
CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases. (2)
CC HMW-kininogen plays an important role in blood coagulation by
CC helping to position optimally prekallikrein and factor XI next to
CC factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
CC induced aggregation of thrombocytes; (4) the active peptide
CC bradykinin that is released from HMW-kininogen shows a variety of
CC physiological effects; (4A) influence in smooth muscle
CC contraction, (4B) induction of hypotension, (4C) natriuresis and
CC diuresis, (4D) decrease in blood glucose level, (4E) it is a
CC mediator of inflammation and causes (4E1) increase in vascular
CC permeability, (4E2) stimulation of nociceptors (4E3) release of
CC other mediators of inflammation (e.g. prostaglandins), (4F) it has
CC a cardioprotective effect (directly via bradykinin action,
CC indirectly via endothelium-derived relaxing factor action); (5)
CC LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
CC kininogen is in contrast to HMW-kininogen not involved in blood
CC clotting.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular.
CC -1- ALTERNATIVE PRODUCTS:
CC Name=HMW;
CC Name=LMW;
CC IBOID=P01044-1; Sequence=Displayed;
CC Name=LMW;

[illegible]

Query Match 71.2%: Score 477; DB 1; Length 621;
 Best Local Similarity 71.9%; Pred. No. 4.6e-35;
 Matches 87; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

DB 4 KDFVQPTKICVCGPRDIPNPSLEBTLTHITIKNAENNAFFPKIDVKKARVQVA 63
 253 KDFVQPTKICVCGPRDIPNPSLEBTLTHITIKNAENNAFFPKIDVKKARVQVA 312

DB 64 GKXFFIDPVARETTCSESNBELTESCTKGLQSLDCNAEYVYVPEKKIYPTVNCPL 123
 313 GLKXSIYFIARETTCSESNBELTESCTKGLQSLDCNAEYVYVPEKKIYPTVNCPL 372

DB 124 G 124
 373 G 373

RESULT 5
 KNG2_BOVIN STANDARD; PRT; 619 AA.

ID AC P01045; P01047;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Kiningogen-2 precursor (Kiningogen II) (thiol proteinase inhibitor)
 DE [containing: Kiningogen-2 heavy chain; Bradykinin (kallidin I); Lysyl-bradykinin (kallidin II); Kiningogen-2 light chain].
 GN Name=KNG2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM HMW).
 RX MEDLINE=4014106; PubMed=6571699;
 RA Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.;
 RT "A single gene for bovine high molecular weight and low molecular weight kiningogens.";
 RN Nature 305:545-549(1993).
 RL [2]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM LMW).
 RX MEDLINE=83117859; PubMed=6572010.
 RA Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.;
 RT "Primary structures of bovine liver low molecular weight kiningogen precursors and their two mRNAs.";
 RN Proc. Natl. Acad. Sci. U.S.A. 80:90-94(1983).
 RL [3]
 RP PROTEIN SEQUENCE OF 19-376, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=87137530; PubMed=3546295;
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.;
 RT "Bovine high molecular weight kiningogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion.";
 RN J. Biol. Chem. 262:2768-2779(1987).
 RL [4]
 RP PROTEIN SEQUENCE OF 376-391.
 RX MEDLINE=70180420; PubMed=4986212;
 RA Kato H., Nagasawa S., Suzuki T.;
 RT "Studies on the structure of bovine kiningogen: cleavages of disulfide bonds and of methionyl bonds in kiningogen-II.";
 RN J. Biochem. 67:313-323(1970).
 RL [5]
 RP PROTEIN SEQUENCE OF 387-455.
 RX MEDLINE=76260155; PubMed=956151;
 RA Han Y.N., Kato H., Iwanaga S., Suzuki T.;
 RT "Primary structure of bovine plasma high-molecular-weight kiningogen. The amino acid sequence of a glycopeptide portion (fragment 1) following the C-terminus of the bradykinin moiety.";
 RN J. Biochem. 79:1201-1222(1976).
 RL [6]

RP PROTEIN SEQUENCE OF 456-496.
 RX MEDLINE=75170265; PubMed=1169237;
 RA Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
 RT "Studies on the primary structure of bovine high-molecular-weight kiningogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
 RN J. Biochem. 77:55-68(1975).
 RL [7]
 RP CARBOHYDRATE-LINKAGE SITES.
 RA Iwanaga S., Kato H., Sugo T., Ikari N., Hashimoto N., Fujii S.;
 RL (in) Tschesche H., Holzer H. (eds.);
 RL Biological functions of Proteinases, pp.243-259, Springer-Verlag, Berlin (1979).
 RL [8]
 CC -1- FUNCTION: (1) Kiningogens are inhibitors of thiol proteases; (2) HMW-kiningogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kiningogen inhibits the thrombin- and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kiningogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins), (4F) it has a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action); (5) LMW-kiningogen inhibits the aggregation of thrombocytes; (6) LMW-kiningogen is in contrast to HMW-kiningogen not involved in blood clotting.
 CC -1- SUBCELLULAR LOCATION: secreted; extracellular.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=HMW;
 CC IsoId=P01045-1; Sequence=Displayed;
 CC Name=LMW;
 CC IsoId=P01045-2; Sequence=VSP_013564, VSP_013565;
 CC -1- TISSUE SPECIFICITY: plasma.
 CC -1- PTM: Bradykinin is released from kiningogen by plasma kallikrein.
 CC -1- SIMILARITY: Contains 3 cystatin-like domains.
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; V01492; CAA24736.1; -; mRNA.
 CC EMBL; V00427; CAA23710.1; -; mRNA.
 CC PIR; A01282; KGB012.
 CC PIR; A01284; KGB012.
 CC HSP; P01038; I490.
 CC InterPro; IPR002395; Kiningogen.
 CC InterPro; IPR000010; Prot inh_cystat.
 CC Pfam; PF00031; Cystatin; 3.
 CC PRINTS; PR00334; KININOGEN.
 CC SMART; SM00043; CY; 3.
 CC PROSITE; PS00287; CYSTATIN_2.
 CC Alternative splicing; Blood coagulation; Bradykinin;
 CC Direct protein sequencing; Glycoprotein; Hydroxylation;
 CC Inflammatory response; Plasma; Protease inhibitor;
 CC Pyrolytic carboxylic acid; Repeat; Signal; Thiol protease inhibitor;
 CC Vasoactive; Vasodilator.
 CC SIGNAL 1 18
 CC CHAIN 19 619 Kiningogen-2.
 CC CHAIN 19 376 Kiningogen-2 heavy chain.
 CC PEPTIDE 377 386 Lysyl-bradykinin.
 CC PEPTIDE 378 386 Bradykinin.
 CC CHAIN 387 619 Kiningogen-2 light chain.
 CC CHAIN 387 619 Cystatin-like 1.
 CC DOMAIN 19 135 Cystatin-like 2.
 CC DOMAIN 136 256 Cystatin-like 3.
 CC DOMAIN 257 376 Not glycosylated.
 CC SITE 47 47

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FT SITE 376 377 Cleavage (by kallikrein).
FT SITE 386 387 Cleavage (by kallikrein).
FT SITE 496 497 Cleavage (by kallikrein).
FT MOD_RES 19 19 Pyroglutamate carboxylic acid.
FT MOD_RES 380 380 4-Hydroxyproline (By similarity).
FT CARBOHYD 87 87 N-linked (GlcNAc...); partial.
FT CARBOHYD 136 136 O-linked (GlcNAc...); partial.
FT CARBOHYD 168 168 N-linked (GlcNAc...); partial.
FT CARBOHYD 169 169 N-linked (GlcNAc...); partial.
FT CARBOHYD 197 197 N-linked (GlcNAc...); partial.
FT CARBOHYD 204 204 N-linked (GlcNAc...); partial.
FT CARBOHYD 280 280 N-linked (GlcNAc...); partial.
FT CARBOHYD 396 396 O-linked (GlcNAc...); partial.
FT CARBOHYD 397 397 O-linked (GlcNAc...); partial.
FT CARBOHYD 398 398 O-linked (GlcNAc...); partial.
FT CARBOHYD 400 400 O-linked (GlcNAc...); partial.
FT CARBOHYD 404 404 O-linked (GlcNAc...); partial.
FT CARBOHYD 510 510 O-linked (GlcNAc...); partial.
FT CARBOHYD 518 518 O-linked (GlcNAc...); partial.
FT CARBOHYD 522 522 O-linked (GlcNAc...); partial.
FT CARBOHYD 534 534 O-linked (GlcNAc...); partial.
FT CARBOHYD 546 546 O-linked (GlcNAc...); partial.
FT CARBOHYD 551 551 O-linked (GlcNAc...); partial.
FT CARBOHYD 568 568 O-linked (GlcNAc...); partial.
FT DISULFID 27 589 Interchain (between heavy and light chains).

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FT DISULFID 82 93 VSLPMSAPVQDERDSKSGQPTGHDGKQI -> T
FT DISULFID 106 125 HVSCEYKGRPOEAGAPAPGQEVSLPASPQLAR (in
FT DISULFID 141 144 isoform LMW).
FT DISULFID 205 217 /FTid=VSP_013565.
FT DISULFID 228 247 Missing (in isoform LMW).
FT DISULFID 261 264 /FTid=VSP_013565.
FT DISULFID 325 337 T -> P.
FT DISULFID 349 367 L -> V.
FT DISULFID 349 367 H -> K.
FT VARSPLIC 619 AA; 68710 MW; F04320ABEB0E0DA CRC64;

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Query Match 67.2%; Score 450; DB 1; Length 619;
Best Local Similarity 66.9%; Pred. No. 1.6e-33;
Matches 84; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

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QY 3 GKDVPQPTKICVGCPRDIPNPSPELEETLTHTTTKNAENNAATPFKIDNVKKAQVQV 62
DB 252 GEDFL--PPWVCVCPKPIPVDSPLLEALNHSIAKNAEDHGFFYFKIDTVKKAIVQV 309
QY 63 AGKVFIDFVARETTCKESNEBELTESCETKGLGSLDCNAEYVVPWEKKIYPTVNCQ 122
DB 310 GGLKSYIFIRARETTCKESNEBELTESCETKGLGSLDCNAEYVVPWEKKIYPTVNCQ 369
QY 123 LG 124
DB 370 LG 371

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RESULT 6
Q6S911_MOUSE PRELIMINARY; PRT; 480 AA.
AC Q6S911;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE HMW kininogen-I variant (High molecular weight kininogen I isoform
DE Delta5).
GN Name=Kngl1;
OS Mus musculus (Mouse).

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OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RX MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA Cardoso C.C., Garrett T., Cayla C., Meneton F., Pequeño J.B.,
RT "Structure and expression of two kininogen genes in mice."
RL Biol. Chem. 385:295-301 (2004).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Merklov S.M., Komar A.A., McCrae K.R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY462058; AAR88632.1; mRNA.
DR EMBL; AY660571; AAT70087.1; mRNA.
DR MGI; MGI:1097705; Kngl1.
DR GO; GO:0005615; Cytoplasmic space; TAS.
DR InterPro; IPR000010; Prot_inh_cyscat.
DR Pfam; PF00031; Cyscatin; 3.
DR SMART; SM00043; Cy; 3.
DR PROSITE; PS00287; CYSTATIN; 1.
SQ SEQUENCE 480 AA; 53205 MW; 7D0A95F5CA98DE CRC64;

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Query Match 64.8%; Score 434; DB 2; Length 480;
Best Local Similarity 66.1%; Pred. No. 3.8e-32;
Matches 82; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

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QY 2 SGKDFVQPTKICVGCPRDIPNPSPELEETLTHTTTKNAENNAATPFKIDNVKKAQVQV 61
DB 251 SGDDLVEALPKPCGCRDIPVDSPELEKVLGSHINQNAENHPFYKIDTVKKAISQV 310
QY 62 VAKKVFIDFVARETTCKESNEBELTESCETKGLGSLDCNAEYVVPWEKKIYPTVNCQ 121
DB 311 VAGKVFIEIRARETTCKESNEBELTESCETKGLGSLDCNAEYVVPWEKKIYPTVNCQ 370
QY 122 PLGM 125
DB 371 ALDM 374

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RESULT 7
KNG1_MOUSE STANDARD; PRT; 661 AA.
AC 008677; 008676; Q91XK5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Kininogen-1 precursor [Contains: kininogen-1 heavy chain; Bradykinin;
DE kininogen-1 light chain].
GN Name=Kngl1; Synonyms=Kng;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE [RNA] (ISOFORMS HMW AND LMW).
RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;
RX MEDLINE=97342556; PubMed=9199253; DOI=10.1016/S0167-4781(97)00018-3;
RA Takano M., Kondo J., Yajima K., Otani M., Sano K., Okamoto H.;
RT "Molecular cloning of cDNAs for mouse low-molecular-weight and high-
RT molecular-weight prekininogens."
RL Biochim. Biophys. Acta 1352:222-230 (1997).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LMW).
RC STRAIN=C57BL/6J; TISSUE=Placenta;
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kaenaka T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,

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RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kaplan A., Marcude H., Batalov S., Betzel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chochia C., Corradi L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimond S., Guisclair S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedziera R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglocz D.R., Malczis L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilmng L.G., Wyshaw-Boris A., Yamagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiroki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyasaka A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasuniishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LMW).
 RC TISSUE=Liver;
 RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidl T.B., Toobylyki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 RA Buterfield J.S.N., Krzywinski M.I., Skalek U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)
 CC HMW-kininogen plays an important role in blood coagulation by
 CC helping to position optimally prekallikrein and factor XI next to
 CC factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
 CC induced aggregation of thrombocytes; (4) the active peptide
 CC bradykinin that is released from HMW-kininogen shows a variety of
 CC physiological effects: (4A) influence in smooth muscle
 CC contraction, (4B) induction of hypotension, (4C) natriuretic and
 CC diuretic, (4D) decrease in blood glucose level, (4E) it is a
 CC mediator of inflammation and causes (4E1) increase in vascular
 CC permeability, (4E2) stimulation of nociceptors (4E3) release of
 CC other mediators of inflammation (e.g. prostaglandins), (4F) it has
 CC a cardioprotective effect (directly via bradykinin action,
 CC indirectly via endothelium-derived relaxing factor action); (5)
 CC LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
 CC kininogen is in contrast to HMW-kininogen not involved in blood
 CC clotting (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=HMW;
 CC IsoId=O08677-1; Sequence=Displayed;

CC Name=LMW;
 CC IsoId=O08677-2; Sequence=VSP_001263, VSP_001264;
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- PTM: Bradykinin is released from kininogen by plasma kallikrein.
 CC -1- SIMILARITY: Contains 3 cystatin-like domains.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL: D84435; BAA19743.1; -; mRNA.
 DR EMBL: D84415; BAA19742.1; -; mRNA.
 DR EMBL: AK005547; -; NOT ANNOTATED_CDS; mRNA.
 DR EMBL: BC018158; AAH18158.1; -; mRNA.
 DR Ensembl: ENSEMBL0000002875; Mus musculus.
 DR MGI: MGI:1097705; Kngl.
 DR GO: GO:0005615; Cytoplasmic space; TAS.
 DR InterPro: IPR002395; Kininogen.
 DR InterPro: IPR000010; Prot_inh_cytc.
 DR Pfam: PF00031; Cystatin; 3.
 DR PRINTS: PR00334; KININOGEN.
 DR PROSITE: PS00287; CYPSTATIN; 1.
 KM Alternative splicing: Blood coagulation; Bradykinin; Glycoprotein;
 KM Inflammatory response; Plasma; Protease inhibitor; Repeat; Signal;
 KM Thiol protease inhibitor; Vasodilator.
 FT SIGNAL 1 18
 FT CHAIN 19 661
 FT CHAIN 19 379
 FT PEPTIDE 380 388
 FT CHAIN 389 661
 FT DOMAIN 19 135
 FT DOMAIN 136 257
 FT DOMAIN 258 379
 FT COMPIAS 439 524
 FT CARBOHYD 82 82
 FT CARBOHYD 168 168
 FT CARBOHYD 204 204
 FT CARBOHYD 242 242
 FT DISULFID 28 631
 FT DISULFID 83 94
 FT DISULFID 107 125
 FT DISULFID 141 144
 FT DISULFID 205 217
 FT DISULFID 228 247
 FT DISULFID 263 266
 FT DISULFID 327 339
 FT DISULFID 350 369
 FT DISULFID 401 432
 FT VARSPLIC 433 661
 FT VARSPLIC 661 AA; 73102 MM; 774460258058796E CRC64;
 SQ SEQUENCE 661 AA; 73102 MM; 774460258058796E CRC64;
 Query Match 64.8%; Score 434; DB 1; Length 661;
 Best local Similarity 66.1%; Pred. No. 5.3e-12;
 Matches 82; Conservative 11; Mismatches 31; Indels 0; Gaps 0;
 OY 2 SGKDFVQPTTKCVGCPRIPTNSPELTHTTTKLAENNATYFKIDNVKKARVQY 61
 DB 251 SGDDLVEALPKPCGPRIPYDPSPELKEVLGHSIAQLAENDHPYXYIDTVYKATSOV 310
 OY 62 VAGKKVFIDFVAETTSKESNBELESCEYKGGSLGSLDCAEVVVVPEKKIYPTVACO 121
 DB 311 VAGTKVFIEFVARETKSKESNTIELADECEIKHLGSLDCAEVVVVPEKKIYPTVACO 370
 OY 122 PLGM 125
 DB 371 ALDM 374

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RESULT 8
OSM8AO RAT PRELIMINARY; PRT; 433 AA.
ID OSM8AO
AC OSM8AO
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Kngl protein.
GN Name=Kngl;
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
OX
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Liver;
RC MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,
RA Datchenko L., Marnissa K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Tothiyaki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttenfield Y.S.N., Krzywinski M.I., Skalecki U., Smallus D.E.,
RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088155; AAB815.1; -; mRNA.
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
SQ SEQUENCE 433 AA; 47891 MW; 6D584348595165ED CRC64;

Query Match 63.6%; Score 426; DB 2; Length 433;
Best Local Similarity 65.0%; Pred. No. 1.9e-31;
Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

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```

DE Kininogen-1 precursor [Contains: Kininogen-1 heavy chain; Bradykinin;
DE Kininogen-1 light chain].
GN Name=Kngl; Synonyms=Kng;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
OX
[1]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS HMW AND LMW).
RP MEDLINE=87137443; PubMed=3029068;
RX Kitagawa H., Kitamura N., Hayashida H., Miyata T., Nakanishi S.;
RA "Differing expression patterns and evolution of the rat kininogen gene
RT family";
RL J. Biol. Chem. 262:2190-2198(1987).
RN
[2]
RN NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM LMW).
RX MEDLINE=86008264; PubMed=2413018;
RA Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT "Primary structures of the mRNA encoding the rat precursors for
RT bradykinin and T-kinin. Structural relationship of kininogens with
RT major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
RL J. Biol. Chem. 260:12054-12059(1985).
RN
[3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 1-65.
RP STRAIN=Bufalo;
RX MEDLINE=87250580; PubMed=2439509;
RA Fung W.-P., Schreiber G.;
RT "Structure and expression of the genes for major acute phase alpha 1-
RT protein (thioesterin) and kininogen in the rat.";
RL J. Biol. Chem. 262:9298-9308(1987).
RN
[4]
RN NUCLEOTIDE SEQUENCE OF 1-41.
RP STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=87137465; PubMed=3818598;
RA Kageyama R., Kitamura N., Okubo H., Nakanishi S.;
RT "Differing utilization of homologous transcription initiation sites of
RT rat K and T kininogen genes under inflammation condition.";
RL J. Biol. Chem. 262:2345-2351(1987).
RN
[5]
RN FUNCTION: (1) Kininogens are inhibitors of t-lyso proteases; (2)
RN HMW-kininogen plays an important role in blood coagulation by
RN helping to position optimally prekallikrein and factor XI next to
RN factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-
RN induced aggregation of thrombocytes; (4) the active peptide
RN bradykinin that is released from HMW-kininogen shows a variety of
RN physiological effects; (4A) influence in smooth muscle
RN contraction; (4B) induction of hypotension; (4C) natriuretic and
RN diuretic; (4D) decrease in blood glucose level; (4E) it is a
RN mediator of inflammation and causes (4E1) increase in vascular
RN permeability; (4E2) stimulation of nociceptors (4E3) release of
RN other mediators of inflammation (e.g. prostaglandins); (4F) it has
RN a cardioprotective effect (directly via bradykinin action);
RN indirectly via endothelium-derived relaxing factor action); (5)
RN LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-
RN kininogen is in contrast to HMW-kininogen not involved in blood
RN clotting.
RN
[6]
RN SUBCELLULAR LOCATION: Secreted; extracellular.
RN
[7]
RN ALTERNATIVE PRODUCTS:
RN Event=Alternative splicing; Named isoforms=2;
RN Name=HMW;
RN IsoId=P08934-1; Sequence=Displayed;
RN Name=LMW;
RN IsoId=P08934-2; Sequence=VSP_001265, VSP_001266;
RN
[8]
RN TISSUE SPECIFICITY: Plasma.
RN
[9]
RN PTM: Bradykinin is released from kininogen by plasma kallikrein.
RN
[10]
RN MISCELLANEOUS: Rate expresses four types of kininogens: the
RN classical HMW/LMW kininogens and two additional LMW-like
RN kininogens: T-I and T-II.
RN
[11]
RN SIMILARITY: Contains 3 cystatin-like domains.
RN
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its

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CC use as long as its content is in no way modified and this statement is not removed.

CC EMBL; L29428; AAA41486.1; -; mRNA.
 CC EMBL; M11884; AAA41487.1; -; mRNA.
 DR EMBL; M14369; AAA41484.1; -; Genomic DNA.
 DR EMBL; M14369; AAA41485.1; ALT SEQ; Genomic DNA.
 DR EMBL; M14655; AAA41482.1; -; Genomic DNA.
 DR PIR; A25486; A25486.
 DR PIR; A28055; A28055.
 DR HSSP; P01040; IDVD.
 DR RGD; 2980; knq1.
 DR InterPro; IPR002395; Kininogen.
 DR InterPro; IPR000010; Prot_inh_cystat.
 DR InterPro; IPR003243; Prot_inh_125A_B.
 DR Pfam; PF00031; Cystatin; 3.
 DR PRINTS; PR00334; KININOGEN.
 DR ProDom; PD001231; Prot_inh_125A_B; 1.
 DR PROSITE; PS00287; CYSSTATIN; 2.
 KM Alternative splicing; Blood coagulation; Bradykinin; Glycoprotein;
 KM Inflammatory response; Multigene family; Plasma; Protease inhibitor;
 KM Repeat; Signal; Thiol protease inhibitor; Vasodilator; Vasodilator.
 FT SIGNAL 1 18
 FT CHAIN 19 639 Kininogen-1.
 FT CHAIN 19 380 Kininogen-1 heavy chain.
 FT PEPTIDE 381 389 Bradykinin.
 FT CHAIN 390 639 Kininogen-1 light chain.
 FT DOMAIN 19 136 Cystatin-like 1.
 FT DOMAIN 137 258 Cystatin-like 2.
 FT DOMAIN 259 380 Cystatin-like 3.
 FT COMPBIAS 439 514 His-rich.
 FT CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 169 169 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 294 294 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential).
 FT DISULFID 28 609 Interchain (between heavy and light chains) (by similarity).
 FT DISULFID 83 94 By similarity.
 FT DISULFID 107 126 By similarity.
 FT DISULFID 142 145 By similarity.
 FT DISULFID 206 218 By similarity.
 FT DISULFID 229 248 By similarity.
 FT DISULFID 264 267 By similarity.
 FT DISULFID 328 340 By similarity.
 FT DISULFID 351 370 By similarity.
 FT VARSPLIC 402 433 VSPSYLARVQBERDPGNEQPIHGHGWLHAKQ -> RLILNS CEYKGRLLKAGAPAPAPRQAEASTVTP (in isoform LMW)
 FT VARSPLIC 434 639 /FTID=VSP_001265.
 FT CONFLICT 61 61 Missing (in isoform LMW).
 FT CONFLICT 61 61 /FTID=VSP_001266.
 FT SEQUENCE 639 AA; 70933 MW; D3172DF94PF56AF5 CRC64; E -> K (in Ref. 2).
 Query Match 63.6%; Score 426; DB 1; Length 639;
 Best Local Similarity 65.0%; Pred. No. 2,9e-31;
 Matches 80; Conservative 14; Mismatches 29; Indels 0; Gaps 0;
 QY 3 GKDVPQPFKICVGCPRDIPPTNSPELEETLTHITTKLNENNAFFFKIDNVKKARQVY 62
 DB 253 GDDLPFLPEBDCGCCRRNIPVDSPELKEALGHSIAQLNENNTFFFKIDTVKKAISQV 312
 QY 63 AGKKYFIDPVARETTCKESNEBELTSCCTKTKLGSLDCNAEYVVPWEKKIYPTVNCOP 122
 DB 313 AGTKYVIEFARETCKSKESNAELTADCEITKRLGSLDCNANVYMPWEKKVVPYVKCKV 372
 QY 123 LGM 125
 DB 373 LDM 375

RESULT 10

O6S910 MOUSE

ID O6S910_MOUSE PRELIMINARY; PRT; 433 AA.

AC O6S910;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE LMW kininogen-II.

GN Name=knq2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N;

RX MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;

RA Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,

RA Bader M.;

RT "Structure and expression of two kininogen genes in mice.";

RL Biol. Chem. 385:295-301(2004).

DR EMBL; AY462059; AAR8633.1; -; mRNA.

DR MGI; MGI:3027157; Knq2.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

DR InterPro; IPR000010; Prot_inh_cystat.

DR SMART; SM00043; CY; 3.

DR PROSITE; PS00287; CYSSTATIN; 1.

SQ SEQUENCE 433 AA; 47887 MW; C86F7BE91C7FE9C0 CRC64;

Query Match 63.4%; Score 425; DB 2; Length 433;
 Best Local Similarity 66.1%; Pred. No. 2,4e-31;
 Matches 80; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 3 GKDVPQPFKICVGCPRDIPPTNSPELEETLTHITTKLNENNAFFFKIDNVKKARQVY 62

DB 252 GDDLPFLPEBDCGCCRRNIPVDSPELKEALGHSIAQLNENNTFFFKIDTVKKAISQV 311

QY 63 AGKKYFIDPVARETTCKESNEBELTSCCTKTKLGSLDCNAEYVVPWEKKIYPTVNCOP 122

DB 312 AGTKYVIEFARETCKSKESNTELTEDCEITKRLGSLDCNANVYMPWEKKVVPYVKCQA 371

QY 123 L 123

DB 372 L 372

RESULT 11

O6S912 MOUSE

ID O6S912_MOUSE PRELIMINARY; PRT; 462 AA.

AC O6S912;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE HMW kininogen-II variant.

GN Name=knq2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N;

RX MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;

RA Cardoso C.C., Garrett T., Cayla C., Meneton P., Pesquero J.B.,

RA Bader M.;

RT "Structure and expression of two kininogen genes in mice.";

RL Biol. Chem. 385:295-301(2004).

DR EMBL; AY462057; AAR8631.1; -; mRNA.

DR MGI; MGI:3027157; Knq2.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

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DR InterPro; IPR000010; Prot_inh_cystat.
DR Pfam; PF00031; Cystatin; 3.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 1.
SQ SEQUENCE 462 AA; 51052 MW; 2A921AB50741C1DC CRC64;

Query Match
Best Local Similarity 63.4%; Score 425; DB 2; Length 462;
Matches 80; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVCGPRDIPNTSPLEETLTHTITKLNANNATYFFKIDNVKKARVQV 62
DB 252 GDDLVLEALPKPCGCPRIIDVDSPELKEVLSIAQLTENDHPYFKIDTVKKAISQV 311
QY 63 AGKKYFIDFVARETTCSKSNELTESCETKLDGSLDCNAEVYVVPWEKKIYPTNCP 122
DB 312 AGNIVIEFTARETKCSKSNELTEDCEIKHLGSLDCNANVYVRPEMKVIFPVKCOA 371
QY 123 L 123
DB 372 L 372

RESULT 12
Q6S913_MOUSE PRELIMINARY; PRT; 644 AA.
ID Q6S913_MOUSE
AC Q6S913;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE HNM kininogen-II.
GN Name=Kng2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RX MEDLINE=23306569; PubMed=15134344; DOI=10.1515/BC.2004.025;
RA Cardoso C.C., Garrett T., Cayla C., Meneton P., Pasquero J.B.,
RT Bader M.;
RL "Structure and expression of two kininogen genes in mice.";
RL Biol. Chem. 385:295-301(2004).
DR EMBL; AY462056; AAR8630.1; -; mRNA.
DR MGI; MGI:3027157; Kng2.
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR InterPro; IPR000395; Kininogen.
DR InterPro; IPR000010; Prot_inh_cystat.
DR Pfam; PF00031; Cystatin; 3.
DR PRINTS; PR00334; KININOGEN.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 1.
SQ SEQUENCE 644 AA; 71272 MW; 5204B683114F565B CRC64;

Query Match
Best Local Similarity 63.4%; Score 425; DB 2; Length 644;
Matches 80; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVCGPRDIPNTSPLEETLTHTITKLNANNATYFFKIDNVKKARVQV 62
DB 252 GDDLVLEALPKPCGCPRIIDVDSPELKEVLSIAQLTENDHPYFKIDTVKKAISQV 311
QY 63 AGKKYFIDFVARETTCSKSNELTESCETKLDGSLDCNAEVYVVPWEKKIYPTNCP 122
DB 312 AGNIVIEFTARETKCSKSNELTEDCEIKHLGSLDCNANVYVRPEMKVIFPVKCOA 371
QY 123 L 123
DB 372 L 372

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RESULT 13
KNT2_RAT STANDARD; PRT; 430 AA.
ID KNT2_RAT
AC P08932;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
DE (Thioesterin) [contains: T-kininogen II heavy chain; T-kinin; T-kininogen II light chain].
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86008264; PubMed=2413018;
RA Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens with major acute phase protein and alpha 1-cysteine proteinase inhibitor.";
RT J. Biol. Chem. 260:12054-12059(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 5-430, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=86008266; PubMed=2413019;
RA Anderson K.P., Heath B.C.;
RT "The relationship between rat major acute phase protein and the kininogens.";
RT J. Biol. Chem. 260:12065-12071(1985).
CC -1- FUNCTION: Kininogens are plasma glycoproteins with a number of functions: (1) as precursor of the active peptide bradykinin they effect smooth muscle contraction, induction of hypotension and increase of vascular permeability. (2) They play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. (3) They are inhibitor of thiol proteases.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- INDUCTION: In response to an inflammatory stimulant. T-kininogen II synthesis is induced and the plasma concentration of T-kininogen I is raised.
CC -1- PTM: As T-kinin is preceded by a Met instead of an Arg or Lys, it is not released from its precursor by either tissue or plasma kallikrein.
CC -1- MISCELLANEOUS: Rats express four types of kininogens: the classical HMW and LMW kininogens produced by alternative splicing of the same gene, and two additional LMW-like kininogens: T-I and T-II.
CC -1- SIMILARITY: Contains 3 cystatin-like domains.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts in positions 180 and 181.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
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DR EMBL; M1185; AAA41491.1; -; mRNA.
DR EMBL; M11661; AAA41570.1; ALT_FRAME; mRNA.
DR PIR; B28055; B28055.
DR GlycoSuiteDB; P08932; -.
DR Ensembl; ENSRNOG0000030387; Rattus norvegicus.
DR InterPro; IPR000010; Prot_inh_cystat.
DR InterPro; IPR003243; Prot_inh_125A_B.
DR Pfam; PF00031; Cystatin; 3.
DR ProDom; PD001231; Prot_inh_125A_B; 1.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
DR Acute phase; Bradykinin; Direct protein sequencing; Glycoprotein;
KW Multigene family; Plasma; Protease inhibitor; Repeat; Signal;
KW Thiol protease inhibitor; Vasoactive; Vasodilator.

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FT SIGNAL 1 18
FT CHAIN 19 430 T-kininogen II.
FT CHAIN 19 375 T-kininogen II heavy chain.
FT PRETIDE 376 386 T-kinin.
FT CHAIN 387 430 T-kininogen II light chain.
FT DOMAIN 19 135 Cysteatin-like 1.
FT DOMAIN 136 257 Cysteatin-like 2.
FT DOMAIN 258 375 Cysteatin-like 3.
FT CARBOHYD 82 375 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 126 126 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 168 168 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 326 326 N-linked (GlcNAc...) (Potential).
FT DISULFID 28 404 Interchain (between heavy and light chains) (By similarity).
FT DISULFID 83 94 By similarity.
FT DISULFID 107 125 By similarity.
FT DISULFID 141 144 By similarity.
FT DISULFID 205 217 By similarity.
FT DISULFID 228 247 By similarity.
FT DISULFID 263 266 By similarity.
FT DISULFID 327 339 By similarity.
FT DISULFID 350 369 By similarity.
FT CONFLICT 26 27 MD -> LN (in Ref. 1).
FT CONFLICT 28 28 C -> R (in Ref. 2).
FT CONFLICT 55 55 L -> V (in Ref. 1).
FT CONFLICT 61 61 E -> K (in Ref. 1).
FT CONFLICT 166 166 F -> S (in Ref. 1).
FT CONFLICT 179 179 T -> R (in Ref. 1).
FT CONFLICT 193 193 N -> D (in Ref. 2).
FT CONFLICT 212 212 F -> S (in Ref. 1).
FT CONFLICT 229 229 R -> T (in Ref. 1).
FT CONFLICT 233 233 Y -> H (in Ref. 1).
FT CONFLICT 415 415 A -> L (in Ref. 2).
SQ SEQUENCE 430 AA; 47704 MW; D94628D848C81525 CRC64;

Query Match 61.0%; Score 409; DB 1; Length 430;
Best Local Similarity 61.8%; Pred. No. 7.4e-30;
Matches 76; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNPELEETLTHITKLNANNATFYFKIDNVKKARQVY 62
DB 252 GDLFLSLPKKCFPCPKNIIPVDSPELKEALGSHIAQNAQHNLFFPKIDTVKKAQSQV 311
QY 63 AGKVFYDFVARETTSKESNEBELTESCETKKGQSLDCAAVYVWVWEKKIYPTVNCOP 122
DB 312 AGTKYVIEFIARETNSKQNTLTADCTKHGQSLNCANVYMRPWEKVVPTVACOA 371
QY 123 LGM 125
DB 372 LDM 374

RESULT 14
Q5M894 RAT PRELIMINARY; PRT; 430 AA.
AC Q5M894_
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Similar to alpha-1 major acute phase protein prepeptide.
GN Name=NGC108747;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauniger R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Uadin T.B., Tothilyuk S., Caraminci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kesteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC088161; AAH88161.1; -, mRNA.
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR InterPro; IPR000243; Proc_inh_cysstat.
DR InterPro; IPR003243; Proc_inh_125A_B.
DR Pfam; PF00031; Cysteatin/3.
DR ProDom; PD001231; Proc_inh_125A_B; 1.
DR SMART; SM00043; CY; 3.
DR POSITE; PS00287; CYSTATIN; 2.
SQ SEQUENCE 430 AA; 47704 MW; D94628D848C81525 CRC64;

Query Match 61.0%; Score 409; DB 2; Length 430;
Best Local Similarity 61.8%; Pred. No. 7.4e-30;
Matches 76; Conservative 15; Mismatches 32; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVGCPRDIPNPELEETLTHITKLNANNATFYFKIDNVKKARQVY 62
DB 252 GDLFLSLPKKCFPCPKNIIPVDSPELKEALGSHIAQNAQHNLFFPKIDTVKKAQSQV 311
QY 63 AGKVFYDFVARETTSKESNEBELTESCETKKGQSLDCAAVYVWVWEKKIYPTVNCOP 122
DB 312 AGTKYVIEFIARETNSKQNTLTADCTKHGQSLNCANVYMRPWEKVVPTVACOA 371
QY 123 LGM 125
DB 372 LDM 374

RESULT 15
Q7YRP6_PIG PRELIMINARY; PRT; 140 AA.
AC Q7YRP6_
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Low molecular weight kininogen (Fragment).
GN Name=Kng;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=13679312; DOI=10.1093/biolreprod.103.020412;
RA Vonnahme K.A., Fernando S.C., Ross J.W., Ashworth M.D., Desilva U.,
RA Malayer J.R., Gelibert R.D.,
RT "Porcine endometrial expression of kininogen, factor XII, and plasma
RT kallikrein in cyclic and pregnant gilts."
RL Biol. Reprod. 70:132-138 (2004).
EMBL; AY321363; AAP85260.1; -, mRNA.

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DR HSSP; P01038; 1A90.
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
DR InterPro; IPR000010; Prot_inh_cystal.
DR InterPro; IPR003243; Prot_inh_125A_B.
DR Pfam; PF00031; Cystatin; 1.
DR ProDom; PD001231; Prot_inh_125A_B; 1.
DR SMART; SM00043; CY; 1.
FT NON_TER 1
FT 140 140
SQ SEQUENCE 140 AA; 15650 MW; 17783783603F777 CRC64;

Query Match 60.3%; Score 404; DB 2; Length 140;
Best Local Similarity 78.2%; Pred. No. 6.4e-30;
Matches 79; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY	24	NSPELEETLTHITTKLNAENNAFFPKIDNVKARQVAVGKKYFIDFVARETTCSKSN	83
Db	1	DSPDLKEPLNHSIAKLAENNAVFYFKIGPVEKATQVAVGKKYSIVFTARETTCSKSN	60
QY	84	EELTESCETKKLGQSLDCNAEYVVPWEKKIYPTVNCQPIG	124
Db	61	EELTESCEIKKPGQILKCNASVYVVPWEKKIYPTVKCOLLG	101

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Job time : 254 secs